

Expression of Genes in Human Heart

Table 4 (413 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human heart.

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
442	10386	20209		4.41			
871	10797	20647		17.08			
1029	10947			2.14			
1280	11188	21039		7.97			
1597	11501	21361		1.87			
1619	11523	21381		4.97			
1694	11596	21467		1.01			
1715	11616	21485		0.95			
1721	11622	21491		7.45			
1848	11744	21620		0.98			
1935	11830	21713		3.03			
2119	12008	21907		2.62			
2233	12118	22020		2.34			
3149	13074	22875		3.7			
3403	13320	23121		1.52			
3471	13387	23192		8.97			
3513	13429			0.87			
3607	13521	23309		0.99			
4102	14002	23781		1.71			
4164	14064	23838		5.94			
4184	14084	23858		0.89			
4184	14084	23859		0.89			
4242	14141			1.03			
4730	14616	24402		1.76			
4779	14663			0.78			
4976	14851	24617		5.08			
4983	14883	24629		2.07			
5217	15140	24834		1.92			
5217	15140	24835		1.92			
5328	15248			5			
5436	15356			5.89			
5483	15248			4.9			
5509	15427	25490		2.9			
5668	19451	25678		1.6			

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5690	15599	25700	1.41				
5863	15769		1.84				
6382	16244	26404	1.61				
6382	16244	26405	1.61				
6697	16577	26769	1.29				
6942	16820	27012	1.3				
7494	17364	27569	3.58				
7684	17534	27758	1.26				
8070	17961		3.7				
8219	19472	28355	2.31				
8390	18266		2.84				
8666	18555	28840	2.91				
8757	17906	28150	1.73				
8757	17906	28151	1.73				
8792	18606		2.19				
9464	19094		1.62				
9760	19280	25230	2.11				
5691	15600	25701	13.31	9.9E+00 AJ239028.1	NT		Homo sapiens LSS gene, partial exons 15, 16, 17 and 18
6689	16549	26745	1.54	9.8E+00 U32716.1	NT		Haemophilus influenzae Rd section 31 of 163 of the complete genome
7955	17805	28046	1.32	9.6E+00 AF242432.1	NT		Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nrip1) and general transcription factor III polypeptide 2 (Gtf2i2) genes, complete cds
7955	17805	28047	1.32	9.6E+00 AF242432.1	NT		Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nrip1) and general transcription factor III polypeptide 2 (Gtf2i2) genes, complete cds
2631	12499	22389	2.72	9.4E+00 L11433.1	NT		Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2631	12499	22390	2.72	9.4E+00 L11433.1	NT		Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2631	12499	22612	5.91	9.4E+00 AB043785.1	NT		Mus musculus AT3 gene for antithrombin, complete cds
2631	12499	22612	5.91	9.4E+00 AB043785.1	NT		IMMEDIATE-EARLY PROTEIN 1 (IE1) IMMEDIATE-EARLY PHOSPHOPROTEIN PP89
7206	17083	27271	2.97	9.3E+00 P11210	SWISSPROT		Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5239	15163	24932	2.07	9.1E+00 AF095609.1	NT		Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5239	15163	24933	2.07	9.1E+00 AF095609.1	NT		Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5678	15587	25687	5.51	8.9E+00 BE971806.1	EST_HUMAN		601651038RT NIH_MGG_81 Homo sapiens cDNA clone IMAGE:3934592 3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5848	15754	25871	1.71	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster C _o Tbx3 premature mRNA, partial cds
5848	15754	25872	1.71	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster C _o Tbx3 premature mRNA, partial cds
433	10378	20199	1.75	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
7439	16452	26642	3.68	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
8509	18381		2.31	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
6346	16209		2.07	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
6888	16747	26940	1.53	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
6888	16747	26941	1.53	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5544	15460	25531	2.58	7.4E+00	BF700517.1	EST_HUMAN	602128876f1 NIH_3T3 cDNA clone IMAGE:4285566 5'
7085	16962	27155	3.83	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
7085	16962	27156	3.83	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2947	12874	22671	4.2	7.2E+00	L12051.1	NT	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
2947	12874	22672	4.2	7.2E+00	L12051.1	NT	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
6239	16105	26254	1.3	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
6239	16105	26255	1.3	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7535	17386		8.48	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
8690	18577	28860	3.26	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 kDa protein in MRDA-PHPB INTERGENIC REGION
7735	17585	27809	2.98	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
8575	18443	28712	1.85	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS3
6818	16697	26889	2.72	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
7925	17775	28015	1.3	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
6614	16194	26680	1.45	6.8E+00	W03412.1	EST_HUMAN	z07ct11r1 Scates melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291860 5'
6614	16194	26681	1.45	6.8E+00	W03412.1	EST_HUMAN	z07ct11r1 Scates melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291860 5'
7277	17154		1.47	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEINS VP5 AND VP8]
7883	17713	27957	3.82	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 kDa PROTEIN C38C10.5 IN CHROMOSOME II
7796	17846	27881	2.1	6.6E+00	Q92E07	SWISSPROT	URIDYLATE KINASE (UK) (URIDYL MONOPHOSPHATE KINASE) (UMP KINASE)
7796	17846	27882	2.1	6.6E+00	Q92E07	SWISSPROT	URIDYLATE KINASE (UK) (URIDYL MONOPHOSPHATE KINASE) (UMP KINASE)
8471	18344		2.17	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C6C3.05G
7236	17172	27372	8.32	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
7616	17467	27696	1.44	6.2E+00	AY010901.1	NT	Schizosaccharomyces pombe unknown mRNA
5928	15633	25956	7.16	5.9E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K ⁺ channel subunit (Kcnk6) genes, complete cds
3479	13395		0.81	5.8E+00	7661557	NT	Homo sapiens DESC1 protein (DESC1), mRNA

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8770	17919	28166	2.44	5.6E+00	Q55276	SWISSPROT	LYCOPENE BEATA CYCLASE
8769	17918	28165	2.65	5.5E+00	P11980	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIS)
8987	18773		1.94	5.5E+00	AL161571.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 67
6593	16473		1.62	5.4E+00	Q91062	SWISSPROT	VITELLOGENIN PRECURSOR (Vtg) [CONTAINS: LIPOVITELLIN LV-1; LIPOVITELLIN LV-2]
7769	17619	27849	1.44	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
7769	17619	27850	1.44	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4675	14561	24354	1.54	5.3E+00	L4326.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6710	16590		4.04	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8899	18708	29003	3.21	5.3E+00	Q27905	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
7655	17505	27730	1.21	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
7989	17809	28050	3.06	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
8610	18477	28749	10.53	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
3972	13879		9.43	4.8E+00	AF185255.1	NT	Eunice australis histone H3 (H3) gene, partial cds
6970	16847		5.01	4.8E+00	AW750067.1	EST HUMAN	PM0-BT0547-3-10100-002-b04 BT0547 Homo sapiens cDNA
286	10251	20071	2.03	4.7E+00	BF240552.1	EST HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716.5'
287	10251	20071	1.92	4.7E+00	BF240552.1	EST HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716.5'
3236	13160	22958	4.01	4.7E+00	AL165280.2	NT	Homo sapiens chromosome 21 segment HS21C030
6576	16434	26617	1.48	4.6E+00	U675589.1	NT	Methanococcus jannaschii section 111 of 150 of the complete genome
8881	18693	28986	1.99	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
3003	12931	22723	0.96	4.4E+00	BF530893.1	EST HUMAN	6020272585F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284.5'
3003	12931	22724	0.96	4.4E+00	BF530893.1	EST HUMAN	6020272585F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284.5'
5764	15671		1.55	4.4E+00	X13414.1	NT	Murine I gene for MHC class II ^a associated invariant chain
6398	16259	26120	2.01	4.3E+00	Y13402.1	NT	Plasmodium falciparum R28R+var1 gene, exon 1
8235	18116	28368	7.49	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5387	15306		2.92	4.2E+00	P16444	SWISSPROT (RDP)	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL Dipeptidase)
6060	16043	26186	1.57	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6060	16043	26187	1.57	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
7182	17059	27249	5.45	4.2E+00	AI89013.1	EST HUMAN	Wf67903_x1 Seares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2380692.3'
6517	16376	26553	7.85	4.1E+00	C23810	SWISSPROT	YY1 PROTEIN PRECURSOR
6577	16435	26618	3.31	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
6577	16435	26619	3.31	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN

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6617	16497	26684	2.95	4.1E+00 U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus	
7576	17427	27641	2.31	4.1E+00 BF892425.1	EST_HUMAN	602247982F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'	
8259	18139		2.89	4.1E+00 P08716	SWISSPROT	HYPOTHETICAL PROTEIN HVLF1	
8339	18216		12.46	4.1E+00 BE885880.1	EST_HUMAN	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909051 5'	
9672	19231	25241	1.86	4.1E+00 P47876	SWISSPROT	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (IGF-BINDING PROTEIN 1)	
6266	16131	26285	1.37	4.0E+00 O35010	SWISSPROT	CELL DIVISION PROTEIN FITSY HOMOLOG	
8768	17917	28164	2.17	4.0E+00 P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III	
8835	18648	28934	3.34	4.0E+00 P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]	
8835	18648	28935	3.34	4.0E+00 P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]	
3459	13375	23181	3.89	3.9E+00 XE4518.1	NT	N.tabacum chitinase gene 50 for class I chitinase C	
4226	14124		0.99	3.9E+00 AF05466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MvSP99) gene, promoter region	
5471	15391	25454	2.47	3.9E+00 BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA	
5471	15391	25455	2.47	3.9E+00 BE814357.1	EST_HUMAN	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION	
6108	16002	26140	4.46	3.9E+00 P39229	SWISSPROT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2	
6355	16218	26379	4.68	3.9E+00 M23907.1	NT	X.laevis mRNA for M4 muscarinic receptor	
6840	16719	26913	2.32	3.9E+00 XE5835.1	NT	Homo sapiens NF2 gene	
8695	17879	28120	3.09	3.9E+00 Y18000.1	NT	mr18af2.s1 NC_OGAP_Ev1 Homo sapiens cDNA clone IMAGE:1168318 similar to gb:A10416	
8715	18532	28816	5.58	3.9E+00 AA861489.1	EST_HUMAN	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN);	
2588	12459		2.4	3.8E+00 AE001562.1	NT	Helicobacter pylori, strain J98 section 123 of 132 of the complete genome	
6911	16789	26982	1.18	3.8E+00 D44725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone IMAGE:14277748 5'	
3936	13845	23622	10.09	3.7E+00 AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39	
8730	18586	28872	2.13	3.7E+00 BF569279.1	EST_HUMAN	60212051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'	
8730	18586	28873	2.13	3.7E+00 BF569279.1	EST_HUMAN	60212051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'	
578	10516	20322	2.1	3.6E+00 AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBU1E10 5'	
7022	16389	27050	3.66	3.6E+00 AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome	
7022	16389	27091	3.66	3.6E+00 AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome	

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8228	18110			3.76	3.6E+00 M96795.1	NT	Escherichia coli glycerophosphate dehydrogenase (glpD) gene, partial cds; and the translation start site has been verified (glpE), the translation start site has been verified (glpG), and repressor protein (glpR) genes, complete cds
3209	13133	22934	1.04	3.5E+00 AF221538.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds	
1496	11400	21260	3.57	3.4E+00 AF254577.1	NT	Brassica napus RPB6d mRNA, complete cds	
2532	12406	22298	1.02	3.4E+00 AL153278.2	NT	Homo sapiens chromosome 21 segment HS21C073	
6354	16217	26378	2.41	3.4E+00 P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT	
7889	17739	27982	3.17	3.4E+00 AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds	
8818	18631	28919	1.92	3.4E+00 L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end	
5036	14908	24679	1.41	3.3E+00 7662155	NT	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA	
5036	14908	24680	1.41	3.3E+00 7662155	NT	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA	
492	10435	20248	1.39	3.2E+00 X96422.1	NT	D. rerio zp-50 POU gene	
3938	10435	20248	0.79	3.2E+00 X96422.1	NT	D. rerio zp-50 POU gene	
5439	15359	25415	2.68	3.2E+00 P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC	
5439	15359	25416	2.66	3.2E+00 P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC	
5508	15713	25525	2.06	3.2E+00 P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4	
5608	15713	25526	2.06	3.2E+00 P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4	
6569	16427	26609	2.35	3.2E+00 Y13685.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes	
6569	16427	26610	2.35	3.2E+00 Y13685.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes	
7221	17098		6.33	3.2E+00 P13061	SWISSPROT	PERIPLASMIC NIFEF HYDROGENASE SMALL SUBUNIT (NFE HYDROGENASE SMALL CHAIN)	
7491	17361	27587	1.17	3.2E+00 M36383.1	NT	S. cerevisiae threonine deaminase (LVL1) gene, complete cds	
7837	17687	27932	1.69	3.2E+00 AB016081.2	NT	Oryza sativa L. genes for guanylyl cyclase C, complete cds	
9089	18863		4.32	3.2E+00 L33336.1	NT	Sus scrofa choline acetyltransferase gene, promoter region	
5582	15497	25574	2.42	3.1E+00 Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C22E2.02 IN CHROMOSOME I	
7000	16877	27067	4.35	3.1E+00 P49384	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE)(DIO1) (TYPE 1 DI) (5DI)	
7000	16877	27068	4.35	3.1E+00 P49384	SWISSPROT	TYPE II IODOTHYRONINE DEIODINASE (TYPE-II 5'DEIODINASE)(DIO2) (TYPE 1 DI) (5DI)	
7334	17238		3.8	3.1E+00 Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2G) (NR2C) (NMDAR2C)	
7920	17770	28009	4.78	3.1E+00 P49385	SWISSPROT	DEOXYHYDROSYNTHASE (DHs)	
8159	17908		3.78	3.1E+00 P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]	
8774	18591		3.35	3.1E+00 S56660.1	NT	retinoic acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]	

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2807	12737	22535	1.06	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
5273	15195	24970	1.63	3.0E+00	X53096.1	NT	Saureus genes encoding Saug961 DNA methyltransferase and Saug961 restriction endonuclease
6245	16111		9.5	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7164	17041		1.45	3.0E+00	X67388.1	NT	B.napus DNA for myrosinase
8374	18251	28501	6.51	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
8374	18251	28502	6.51	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
1964	11858	21747	2.58	2.9E+00	AE02225.2	NT	Chlamydomonas reinhardtii AR39, section 53 of 94 of the complete genome
6129	15976	26112	1.63	2.9E+00	Z36819.1	NT	F.principis gcdsPA gene for P-protein of the glycine cleavage system
6282	16146	26300	4.47	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6282	16146	26301	4.47	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6410	16271	26433	5.19	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
1441	11346	21212	5.79	2.8E+00	AF185398.1	NT	Buxus harlandii maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product
1615	11159		3.12	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
6325	16188	26350	4.78	2.8E+00	8393724	NT	Mus musculus endomucin (LOC32423), mRNA
230	10199	20012	4.63	2.7E+00	6679306	NT	Mus musculus perhexamer repeat gene 3 (Phxr3), mRNA
230	10199	20013	4.63	2.7E+00	6679306	NT	Mus musculus perhexamer repeat gene 3 (Phxr3), mRNA
5408	15327	25377	1.75	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
7185	17062		2.21	2.7E+00	AL116459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7996	17846		2.16	2.7E+00	BE063527.1	EST_HUMAN	CM0-BT0281-031199-087-f04 BT0281 Homo sapiens cDNA
4576	14467	24253	4.35	2.6E+00	AF068749.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5405	15524	25373	1.97	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5405	15524	25374	1.97	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
6533	16391		5.42	2.6E+00	AF235502.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
6686	16576	26767	1.2	2.6E+00	AJ132180.1	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
6696	16576	26768	1.2	2.6E+00	AJ132180.1	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
7567	17418	27634	2.95	2.6E+00	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
7927	17777		1.52	2.6E+00	Q055193	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
9711	19849		2.31	2.6E+00	11419220	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1448	11353	21216	2.08	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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1448	11353	21217	2.08	2.5E+00 A 271844.1	NT		Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5552	15468	25537	2.33	2.5E+00 P 13485	SWISSPROT		TEICOIC ACID BIOSYNTHESIS PROTEIN F
5552	15468	25538	2.33	2.5E+00 P 13485	SWISSPROT		TEICOIC ACID BIOSYNTHESIS PROTEIN F
5886	15468	25537	1.71	2.5E+00 P 13485	SWISSPROT		TEICOIC ACID BIOSYNTHESIS PROTEIN F
5886	15468	25538	1.71	2.5E+00 P 13485	SWISSPROT		TEICOIC ACID BIOSYNTHESIS PROTEIN F
6561	16419	26598	1.34	2.5E+00 AW949158.1	EST_HUMAN		QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA
7264	17141	27334	1.75	2.5E+00 D50307.1	NT		Rice DNA for addelase C-1, complete cds
9086	18861		2.26	2.5E+00 AF289685.1	NT		Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
2980	12907	22707	0.86	2.4E+00 M 24282.1	NT		Chicken alpha-3 collagen type VI mRNA, 3' end
4816	14659	24485	7.62	2.4E+00 4503352	NT		Homo sapiens double O2-like domains, alpha (DOC2A) mRNA
5657	15559	25664	4.19	2.4E+00 P 2843	SWISSPROT		VITELLOGENIN I PRECURSOR (VOLK PROTEIN 1)
6733	16613	26802	2.14	2.4E+00 P 28842	SWISSPROT		CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
6733	16613	26803	2.14	2.4E+00 P 28842	SWISSPROT		CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
6780	16559		2.63	2.4E+00 AE001486.1	NT		Helicobacter phori, strain J99 section 47 of 132 of the complete genome
7026	16903		1.71	2.4E+00 AW875126.1	EST_HUMAN		RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
7125	17002	27194	9.45	2.4E+00 P 24091	SWISSPROT		ENDOCHITINASE B PRECURSOR (CHN-B)
7771	17621	27853	2.5	2.4E+00 P 13673	SWISSPROT		SKIN GRANULE PROTEIN PRECURSOR
7771	17621	27854	2.5	2.4E+00 P 13673	SWISSPROT		SKIN GRANULE PROTEIN PRECURSOR
7820	17670	27911	2.18	2.4E+00 X 2511.1	NT		H. sapiens CTGF gene and promoter region
7881	17731		6.49	2.4E+00 P 05099	SWISSPROT		XYLOSE KINASE (XYLUOKINASE)
7914	17764	28002	1.67	2.4E+00 BE 26702.1	EST_HUMAN		hr63f06_x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3 133 187_3'
7914	17764	28003	1.67	2.4E+00 BE 26702.1	EST_HUMAN		hr63f06_x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3 133 187_3'
8428	18302	28558	1.77	2.4E+00 Y 4079.1	NT		Bacillus subtilis chromosomal DNA, region 75 degrees: gfpPFKD operon and downstream
8665	18554	28839	2.52	2.4E+00 AF 158552.2	NT		Frangaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1233	11140	20992	9.36	2.3E+00 Z 6724.1	NT		G.domesticus artificial single chain antibody gene (L3)
4031	13834		1.28	2.3E+00 A 401081.1	NT		Bos taurus partial cytb gene for cytochrome b
6408	16259	26431	2.22	2.3E+00 6978554	NT		Rattus norvegicus ATPase, Cat+, transporting, ubiquitous (Atp2a3), mRNA
6479	19766		2.3	2.3E+00 P 07199	SWISSPROT		MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
6573	16431	26613	1.53	2.3E+00 X 60265.1	NT		M.mazei dnaK and dnaJ genes homologues coding for DnaK and DnaJ
7289	17165	27364	1.81	2.3E+00 Q 11127	SWISSPROT		ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
8983	18793	29083	2.6	2.3E+00 BF 541987.1	EST_HUMAN		60269f21FNH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173_5'
8983	18793	29084	2.6	2.3E+00 BF 541987.1	EST_HUMAN		60269f21FNH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173_5'

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9304	19002	253533		4	2.3E+00 BE895237.1	EST_HUMAN	601453673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918633 5'
9836	19405			1.37	2.3E+00 AF281862.1	NT	Neurospora crassa G protein alpha subunit GNA-3 (gna-3) gene, complete cds
4216	14114	23891		3.82	2.2E+00 D677071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4216	14114	23892		3.82	2.2E+00 D677071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5276	15198	24973		10.08	2.2E+00 O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5276	15198	24974		10.08	2.2E+00 O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5696	16605	25707		9.06	2.2E+00 BE250383.1	EST_HUMAN	6009434011 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2859777 3'
5635	15741	25653		3.3	2.2E+00 Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
5978	15882	26005		2.89	2.2E+00 P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
6155	15113			3.14	2.2E+00 AA594574.1	EST_HUMAN	ni95b02.st1 NCI CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3
6486	16344	26514		51.56	2.2E+00 AA446012.1	EST_HUMAN	2x05g10.1r1 Soares_total_fetus_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:785634 5'
7381	17250			11.83	2.2E+00 BE741678.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
7518	19468			2.1	2.2E+00 Q04706	SWISSPROT	TRANSFOSON TY1 PROTEIN A
7783	17633	27865		1.56	2.2E+00 AI290373.1	EST_HUMAN	qmt89b03.x1 Soares_placenta_80days 2NbHFB80gW Homo sapiens cDNA clone IMAGE:1893965 3'
7783	17633	27866		1.56	2.2E+00 AI290373.1	EST_HUMAN	similar to qb:Y00433 GLUTATHIONE_PEROXIDASE (HUMAN);
7812	17662	27902		2.28	2.2E+00 BF246782.1	EST_HUMAN	qmt89b03.x1 Soares_placenta_80days 2NbHFB80gW Homo sapiens cDNA clone IMAGE:1893965 3'
7975	17825	28066		2.88	2.2E+00 AF1834416.1	NT	similar to qb:Y00433 GLUTATHIONE_PEROXIDASE (HUMAN);
8739	17888	28132		4.5	2.2E+00 P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
8889	18700	28995		4.67	2.2E+00 P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
567	12670	20304		6.81	2.1E+00 AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3559	13455			1.19	2.1E+00 AW449366.1	EST_HUMAN	U-H-B13-2aki-e-08-0-JL.s1 NC1 CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6074	16057	26206		3.72	2.1E+00 O70159	SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
6195	15955	26087		4.7	2.1E+00 N2953.1	EST_HUMAN	yy08a10.s1 Soares melanocyte 2NbHIM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654
6348	16826			1.99	2.1E+00 AU123630.1	EST_HUMAN	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000671 5'
1178	11089	2034		1.23	2.0E+00 AF180527.1	NT	Homo sapiens p22Dok1 (DOKDEL) mRNA, complete cds

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1173	11089	20835	1.23	2.0E+00	AF080527.1	NT	Homo sapiens p22Dokel (DOKDEL) mRNA, complete cds
1313	11219	21076	1.43	2.0E+00	AF204927.1	NT	Oryctolagus cuniculus Nat_K+-ATPase beta 1 subunit mRNA, complete cds
1557	11462		3.13	2.0E+00	P25582	SWISSPROT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2102	11991	21890	4.6	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
2102	11991	21891	4.6	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4011	13917	23692	2.09	2.0E+00	AW664496.1	EST_HUMAN	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); hi13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
4011	13917	23693	2.09	2.0E+00	AW664496.1	EST_HUMAN	hi13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
6678	16558	26751	3.8	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6678	16558	26752	3.8	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6678	16558	26753	3.8	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
7170	17047	27237	3.3	2.0E+00	F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
9629	19613	24998	5.81	2.0E+00	5834843	NT	Gallus gallus mitochondrial, complete genome
5437	15357	25412	4.67	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itp1), mRNA
5437	15357	25413	4.67	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itp1), mRNA
6047	15580		2.27	1.9E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
6927	16505	26959	2.58	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
6927	16505	27000	2.58	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
7032	16909		3.36	1.9E+00	BF360206.1	EST_HUMAN	CM3-MT0114-010900-323-h12.MT0114 Homo sapiens cDNA
7156	17033		1.86	1.9E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
3054	12981	22773	1.71	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3082	13009	22799	4.48	1.8E+00	U04356.1	NT	Synechococcus sp. PCCT7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (ctpE) genes, complete cds
3082	13009	22800	4.48	1.8E+00	U04356.1	NT	Synechococcus sp. PCCT7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (ctpE) genes, complete cds
5577	15492		2.22	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
5712	15620	25723	1.9	1.8E+00	BF311999.1	EST_HUMAN	60189754F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5
6043	15946	26078	1.3	1.8E+00	BF305552.1	EST_HUMAN	60189348F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5
7140	17017	27210	2.09	1.8E+00	O43281	SWISSPROT	EMBRYONAL FN-ASSOCIATED SUBSTRATE (HEFS)
7293	17169	27369	1.21	1.8E+00	R31042.1	EST_HUMAN	yh72508.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:135273 5
7899	17749		3.29	1.8E+00	AF411949.1	NT	Homo sapiens PRO0530 mRNA, complete cds
8998	18801		3.76	1.8E+00	P36062	SWISSPROT	HYPOTHETICAL 75.6 kD PROTEIN IN SDH1-CM5/TA3 INTERGENIC REGION

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9428	19584			4.01	1.8E+00 AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
9504	19119			2.4	1.8E+00 9506404 NT	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA	
9968	19429			1.34	1.8E+00 Bf516805.1	EST_HUMAN	601903509F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:1255865'
1092	11008	20849		1.92	1.7E+00 Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2225	12110	22013		3.25	1.7E+00 AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2321	12202	22101		1.02	1.7E+00 AI141067.1	EST_HUMAN	oz33hu5.x1 Soares_NhMPu_S1 Homo sapiens cDNA clone IMAGE:16781373'
4356	14262	24037		0.84	1.7E+00 Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5448	15369	25424		1.48	1.7E+00 BE063545.1	EST_HUMAN	CMD-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5448	15369	25425		1.48	1.7E+00 BE063546.1	EST_HUMAN	CMD-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5664	15575	25673		3.58	1.7E+00 Q91TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF)
7014	16891			1.29	1.7E+00 Bf508000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:41400845'
7282	19467	27355		2.15	1.7E+00 O60479	SWISSPROT	HOMEBOX PROTEIN DLX3
7282	19467	27356		2.15	1.7E+00 O60479	SWISSPROT	HOMEBOX PROTEIN DLX3
8874	18666	28977		1.78	1.7E+00 W22424.1	EST_HUMAN	67B7 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
9384	19044	25306		1.37	1.7E+00 AI678443.1	EST_HUMAN	tu82d07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:22575493' similar to contains MSR1 t1
9860	19351	25185		2.26	1.7E+00 AI198573.1	EST_HUMAN	MSR1 repetitive element;
1989	11882	21775		16.73	1.6E+00 AF198939.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
1997	11891	21783		3.61	1.6E+00 AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2003	11896	21788		1.96	1.6E+00 Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
2238	12122			1.48	1.6E+00 X88373.1	NT	B.napus gene encoding endo-polygalacturonase
2931	12858	22658		2.52	1.6E+00 W58426.1	EST_HUMAN	zg25f01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:3416895' similar to
3946	13854			5.14	1.6E+00 BE570077.1	EST_HUMAN	gb:D29805 NACETYLGLUCOSAMINE SYNTHASE (HUMAN);
4255	14154	23928		1.44	1.6E+00 AF55827.1	NT	602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:43105913'
4255	14154	23929		1.44	1.6E+00 AF55827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5016	14890	24657		3.14	1.6E+00 Y11344.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5016	14890	24658		3.14	1.6E+00 Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5558	15474	25546		2.19	1.6E+00 L04898.1	NT	Brachydanio rerio MHC class II Da-beta-2'01 gene, 3' end
6296	16160	26317		2.64	1.6E+00 BE997287.1	EST_HUMAN	RCO-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6681	16361		1.21	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
6881	16760	26968	3.56	1.6E+00	AJ297131.1	NT	Mus musculus S1L, MAP_17, CYP_a, SCL & CYP_b genes
7444	19465	266646	1.3	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-1
7444	19465	266647	1.3	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-1
7611	17462	27679	1.29	1.6E+00	T41290.1	EST_HUMAN	phob6_19j1TV Outward Alu-primed hnRNA library Homo sapiens cDNA clone phob6_19j1TV
7882	17702	27946	1.25	1.6E+00	AW385644.1	EST_HUMAN	QV4-LT0016-09/0200-100-d07 LT0016 Homo sapiens cDNA
7882	17702	27947	1.25	1.6E+00	AW385644.1	EST_HUMAN	QV4-LT0016-09/0200-100-d07 LT0016 Homo sapiens cDNA
8217	15520	25601	5.86	1.6E+00	AF056531.1	NT	Homo sapiens transglutaminase type 1 (Tgase1) gene, promoter region
8944	18752	29047	3.25	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
9902	19879		1.65	1.6E+00	AV764043.1	EST_HUMAN	AV764043 MDS Homo sapiens cDNA clone MDSDA-H08 5'
30	10017	19812	4.29	1.5E+00	U53449.1	NT	Rattus norvegicus Jun dimerization protein 2 (Jdp-2) mRNA, complete cds
231	10200	20014	1.76	1.5E+00	AE022201.2	NT	Chlamydophila pneumoniae AR39, section 32 of 94 of the complete genome
605	10541		1.79	1.5E+00	6752961	NT	Mus musculus disintegrin and metalloproteinase domain (ADAM) 15 (metarginidin) (Adam15), mRNA
2359	12239	22135	2.46	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2468	12344	22237	2.02	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3099	12239	22135	2.22	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3329	13249	23054	0.82	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5886	15762	25880	2.71	1.5E+00	R17879.1	EST_HUMAN	y910e021r1 Soares infant brain 1NIb Homo sapiens cDNA clone IMAGE:31683 5'
6230	16096		1.42	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH MGIC_68 Homo sapiens cDNA clone IMAGE:3381665 5'
6250	16116	26268	29.13	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
6250	16116	26269	29.13	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7671	17521	27747	7.56	1.5E+00	BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-905 TN0078 Homo sapiens cDNA
7782	17632		1.71	1.5E+00	BF337944.1	EST_HUMAN	602035771F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183865 5'
7886	17706	27951	1.96	1.5E+00	AA017689.1	EST_HUMAN	Z638g06.r1 Seares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
7886	17706	27952	1.96	1.5E+00	AA017689.1	EST_HUMAN	Z638g06.r1 Seares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
8702	18520	28802	3.91	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243_s1_547 (synonym: fibf1) Homo sapiens cDNA clone DKFZp547P243 5'
8828	18641		10.73	1.5E+00	X07350.1	NT	Malte mitochondrial tRNA-Ser gene and tRNA-Rhe pseudogene
9223	18846		1.5	1.5E+00	6753287	NT	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA
9596	19178		2.89	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
9690	19243		1.42	1.5E+00	6978492	NT	Rattus norvegicus 5'-Lipoxygenase (Alox5), mRNA
27	10014	19808	1.28	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
27	10014	19809	1.28	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2231	12116		0.95	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2286	12169			9.38	1.4E+00 U67922.1	NT	Ovis aries prion protein gene, complete cds
2634	12501	22394		1.63	1.4E+00 X74463.1	NT	Human papillomavirus type 7 genomic DNA
2746	12608	22500		3.29	1.4E+00 AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2746	12608	22501		3.29	1.4E+00 AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3034	12962	22755		1.01	1.4E+00 AE002324.2	NT	Chlamydia muridarum, section 55 of 85 of the complete genome
3034	12962	22756		1.01	1.4E+00 AE002324.2	NT	Chlamydia muridarum, section 55 of 85 of the complete genome
3291	13213			0.87	1.4E+00 5453733 NT	Hom sapiens Mad4 homolog (MAD4) mRNA	
4162	14062	23835		1.09	1.4E+00 AW900455.1	EST_HUMAN	CM0-NIN1005-140300-286-h06 NN 005 Homo sapiens cDNA
4162	14062	23836		1.09	1.4E+00 AW900455.1	EST_HUMAN	CM0-NIN1005-140300-286-h06 NN 005 Homo sapiens cDNA
4482	14316			1.53	1.4E+00 BF081547.1	EST_HUMAN	602156687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
5137	15004			0.8	1.4E+00 Q07869	SWISSPROT	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)
5301	15222	25026		1.51	1.4E+00 AW054976.1	EST_HUMAN	wt45g07_x1_NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5394	15313			5.17	1.4E+00 AB032983.1	NT	Hom sapiens mRNA for KIAA1157 protein, partial cds
5796	15702	25812		2.39	1.4E+00 Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
5802	19765			4.9	1.4E+00 AB020712.1	NT	Hom sapiens mRNA for KIAA0905 protein, complete cds
5860	15766	25884		2.71	1.4E+00 Q927777	SWISSPROT	SYNAPSIN II
5860	15766	25885		2.71	1.4E+00 Q927777	SWISSPROT	SYNAPSIN II
6318	16181	26341		1.86	1.4E+00 AJ13269.1	NT	Hom sapiens caveolin-1/-2 locus, Config1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7107	16984			5.21	1.4E+00 A1271735.1	NT	Hom sapiens Xq pseudautosomal region; segment 1/2
7256	17133	27325		1.88	1.4E+00 R20459.1	EST_HUMAN	yg53f12.r1 Soares infant brain 1NIH Homo sapiens cDNA clone IMAGE:34345 5'
7303	17179	27381		3.37	1.4E+00 BE04667.1	EST_HUMAN	RC1-BT0313-301299-012-705 BT0313 Homo sapiens cDNA
8420	18294	28548		1.94	1.4E+00 AA195528.1	EST_HUMAN	z336e09.r1 Soares_NhIMPU_S1 Homo sapiens cDNA clone IMAGE:665512 5' similar to contains element MER22 repetitive element;
8556	18426	28695		4.97	1.4E+00 AB006682.1	NT	Homo sapiens APECED mRNA for AIRE-1, complete cds
8709	18526	28808		5.15	1.4E+00 BE062107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
8709	18526	28809		5.15	1.4E+00 BE062107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
8727	18583	28867		2.68	1.4E+00 U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
8727	18583	28868		2.68	1.4E+00 U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
9221	19604			1.34	1.4E+00 AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12

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553	10498			1.67	1.3E+00 Z73640.1	NT	M.mucedo gene encoding 4-Dihydromethyl-trisporate dehydrogenase
884	10810	20659		2.74	1.3E+00 A1271192.1	NT	Cantharellus sp. partial 2SS rRNA gene, isolate Tibet
1113	11028			16.5	1.3E+00 Y192213.1	NT	Homo sapiens putative psfHba pseudogene for hair keratin, exons 2 to 7
1275	11183	21033		10.9	1.3E+00 4507998	NT	Homo sapiens zinc finger protein 157 (H-ZF22) (ZNF157) mRNA
1275	11183	21034		10.9	1.3E+00 4507998	NT	Homo sapiens zinc finger protein 157 (H-ZF22) (ZNF157) mRNA
1334	11241			1.62	1.3E+00 U817730.2	NT	Cox lacryme-joli dihydrodipicolinate synthase (daps) gene, complete cds
1593	11497			2.09	1.3E+00 AE022388.2	NT	Chlamydias muridarum, section 66 of 85 of the complete genome
2196	12083			2.1	1.3E+00 AB030447.1	NT	Cyprinus carpio MRPb and MASPB genes for mannose-binding lectin-associated serine protease (MASP)
2503	12378			2.19	1.3E+00 BE067135.2	EST_HUMAN	and MASP-related protein, complete cds
2909	12835	22632		1.12	1.3E+00 6755621	NT	60166123R1 NIH MGIC_72 Homo sapiens cDNA clone IMAGE3915945 3'
3547	13463	23258		1.03	1.3E+00 AF016194.1	NT	Mus musculus alpha-spectrin 1, erythroid (Spn1), mRNA
4502	12835	22632		0.82	1.3E+00 6755621	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (AMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
4964	14839	24607		0.98	1.3E+00 A1252087.1	NT	Mus musculus alpha-spectrin 1, erythroid (Spn1), mRNA
4964	14839	24608		0.98	1.3E+00 A1252087.1	NT	Plasmoidium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5665	15576	25674		7.76	1.3E+00 AW352834.1	EST_HUMAN	Plasmoidium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5665	15576	25675		7.76	1.3E+00 AW352834.1	EST_HUMAN	PM0-CT0259-291199-004-04-08 CT0259 Homo sapiens cDNA
5864	15770	25889		1.33	1.3E+00 M33496.1	NT	PM0-CT0259-291199-004-04-08 CT0259 Homo sapiens cDNA
6828	16707	26901		1.25	1.3E+00 A1009812.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6917	16795	26988		3.06	1.3E+00 BE963379.2	EST_HUMAN	Sus scrofa pip gene
7064	16931			1.55	1.3E+00 9910247	NT	601657145R1 NIH MGIC_67 Homo sapiens cDNA clone IMAGE3866195 3'
7480	17350			5.44	1.3E+00 AF042084.1	NT	Homo sapiens GL004 protein (GL004), mRNA
7487	17357	27560		2.31	1.3E+00 X72019.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
7487	17357	27561		2.31	1.3E+00 X72019.1	NT	Saliba phr-1 mRNA for photolyase
7574	17425	27639		1.45	1.3E+00 Q00754	NT	Saliba phr-1 mRNA for photolyase
7620	17471	27630		1.27	1.3E+00 A19277629.1	EST_HUMAN	LYSOSOMAL ALPHA-MANNOSEIDASE PRECURSOR (MANNOSEIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSEIDASE) (LAMAN)
7675	17525	27751		4.9	1.3E+00 BE963379.2	EST_HUMAN	wo35a07_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE2462100 3'
7866	17716	27961		1.6	1.3E+00 AE004292.1	NT	601657145R1 NIH MGIC_67 Homo sapiens cDNA clone IMAGE3866195 3'
7874	17724	27958		1.39	1.3E+00 M20953.1	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
8078	17969			4.3	1.3E+00 Q14117	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
8277	18157	28398		2.34	1.3E+00 P25299	NT	Dihydrodorpyrimidinase (DHPase) (HYDANTOINASE) (DHP)
							SWISSPROT MRNA 3'-END PROCESSING PROTEIN RNA15

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar ('Top') Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8298	18178	28424	2.23	1.3E+00	Z18892.2	NT	Mus musculus desmin gene
8646	18510		1.81	1.3E+00	AW274791.1	EST_HUMAN	xp098e3.x1 NCI_CGAP_HNG Homo sapiens cDNA clone IMAGE:2739868_3'
8826	18659	28923	2.82	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
8895	18705	28999	2.71	1.3E+00	Z28682.1	NT	Bacillus subtilis genomic DNA 23.9kB fragment
9362	19033		2.35	1.3E+00	AF4187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNU12) gene, complete cds
9553	19139	25293	3.24	1.3E+00	BT5348043.1	EST_HUMAN	602023185f1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158452_5'
9544	19499		2.68	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
634	10571	20384	8.14	1.2E+00	AA876246.1	EST_HUMAN	z12208.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535_3'
806	10735	20578	1.33	1.2E+00	PO5228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFIHRP-III)
806	10735	20579	1.33	1.2E+00	PO5228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFIHRP-III)
806	10735	20580	1.33	1.2E+00	PO5228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFIHRP-III)
860	10786		2.19	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PR03077 (PR03077), mRNA
1145	11058	20901	5.53	1.2E+00	AF080246.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1187	11097	20943	1.77	1.2E+00	A1252242.1	NT	pea seed-borne mosaic virus complete genome
1187	11097	20944	1.77	1.2E+00	A1252242.1	NT	pea seed-borne mosaic virus complete genome
1963	11857	21746	1.05	1.2E+00	AF140681.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3072	12999	22759	0.95	1.2E+00	AB050681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3128	13053	22861	5.41	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3128	13053	22862	5.41	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3249	13472		2.9	1.2E+00	PS4910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3311	13232	23038	0.78	1.2E+00	AF183740.1	NT	Homo sapiens Lhx3 gene, intron 2
3312	13233		0.99	1.2E+00	M81779.1	NT	G_gallus T-cadherin mRNA, complete cds
3650	13564	23350	7.28	1.2E+00	U75921.1	NT	Mus musculus subtilisin-like serine protease Lpc (Pc7) gene, exons 1 to 9, partial cds
3904	13814	23598	1.49	1.2E+00	BF5733570.1	EST_HUMAN	MR0-FT075-050900-203-gr06_1 FT0175 Homo sapiens cDNA
4201	13232	23038	1.09	1.2E+00	AF188740.1	NT	Homo sapiens Lhx3 gene, intron 2
4238	14196	23981	1.39	1.2E+00	6980951	NT	Rattus norvegicus Glycine receptor alpha 2 subunit (glycine receptor, neonatal) (Gira2), mRNA
4371	14267		1.64	1.2E+00	M87060.1	NT	Rattus rattus cardiac A53 gene, exons 1-23
4422	14316	24102	1.26	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4460	14354	24145	1.82	1.2E+00	AF156895.1	NT	Homo sapiens post-synaptic density 95 (DlG4) gene, complete cds
4485	14379		5.44	1.2E+00	Y09200.1	NT	T_pinnatum chloroplast tbd_ gene, partial
4584	13233		0.94	1.2E+00	M81779.1	NT	G_gallus T-cadherin mRNA, complete cds
5409	15329	25319	1.96	1.2E+00	AW813276.1	EST_HUMAN	MR3-T0191-140200-013-c05 ST0191 Homo sapiens cDNA
5739	15647	25753	2.47	1.2E+00	X74885.1	NT	D_hydei av1 repeat cluster DNA, fragment D
5769	15676	25753	3.28	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0050-270400-190-ad3 BN0050 Homo sapiens cDNA

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5798	15704	25815	1.87	1.2E+00	X89084.1	NT	C. glutamicum pta gene and ackA gene
5798	15704	25816	1.87	1.2E+00	X89084.1	NT	C. glutamicum pta gene and ackA gene
5823	15729	25841	32.83	1.2E+00	AAV759254.1	EST_HUMAN	ah84g12.s1 Soares testis_NHT Homo sapiens cDNA clone 13222374 3'
5918	15823	25949	1.82	1.2E+00	AW813276.1	EST_HUMAN	MR3_ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6139	15986	26121	2.55	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
6369	19463	26392	1.9	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cda Homo sapiens cDNA clone cdAAFF03 5'
6508	16367	26544	2.4	1.2E+00	X74207.1	NT	L.lactis pyIF and pyF genes
6984	16861	27055	3.45	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
7218	17095	27285	1.74	1.2E+00	AW377210.1	EST_HUMAN	MR2-CT0222-201089-001-e07 C70222 Homo sapiens cDNA
7407	17274	27480	3.08	1.2E+00	Z32850.1	NT	R.communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
7540	17391	27601	1.8	1.2E+00	D11745.1	EST_HUMAN	HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
7711	17581	27786	3.28	1.2E+00	X86832.1	NT	H.sapiens ENO3 gene for muscle specific endolase
8653	18542	28826	2.03	1.2E+00	AW817817.1	EST_HUMAN	PM0-ST0254-161199-001-d01 ST0264 Homo sapiens cDNA
8689	18576		23.47	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
8752	17901	28145	4.87	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
9114	18377	28787	2.5	1.2E+00	AF065398.1	NT	Mus musculus 60 kDa ribonucleoprotein SSA/Ro gene, complete cds
9330	19572	25067	15.4	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9349	19025		1.49	1.2E+00	AP01515.1	NT	Bacillus halodurans genomic DNA, section 9/14
456	10400	20217	1.13	1.1E+00	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1726	11627	21496	1.39	1.1E+00	AW905393.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1857	11753	21628	0.92	1.1E+00	AW575889.1	EST_HUMAN	Ui-HF-BR0-p-alk-f02-0-U1_s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834-3'
3288	13209	23009	6.61	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3288	13209	23010	6.61	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3441	13358	23165	0.93	1.1E+00	8922641 NT	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3510	13426		1.26	1.1E+00	8922973 NT	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
3531	13447	23244	0.99	1.1E+00	AI808360.1	EST_HUMAN	wf54h11.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2355461 3' similar to SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3657	13571	23357	1.16	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of the complete genome
3657	13571	23358	1.16	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of the complete genome
3678	13592	23378	17.81	1.1E+00	5729757 NT	NT	Homo sapiens calpain 9 (nCl-4) (CAPN9) mRNA
3862	13773	23565	0.98	1.1E+00	8922641 NT	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4122	14022		5.89	1.1E+00	5835331 NT	NT	R.unicornis complete mitochondrial genome
4860	14740	24520	1.18	1.1E+00	L23195.1	NT	Drosophila melanogaster cytoplasmic dynein heavy chain mRNA, complete cds
4921	14800	24573	2.92	1.1E+00	U18466.1	NT	African swine fever virus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4999	14874	24638	1.16	1.1E+00	X78425.1	NT	<i>E. faecalis</i> pbp5 gene
5249	15172	24945	1.57	1.1E+00	6978530 NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA	
5449	15370	25426	12.04	1.1E+00	BE960184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826835 3'
5460	15380	25440	1.29	1.1E+00	AI138582.1	EST_HUMAN	qd85c3.x1 Scares._NHT Homo sapiens cDNA clone IMAGE:1736260 3'
6422	16283	26444	1.93	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6422	16283	26445	1.93	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6435	16236	26468	7.53	1.1E+00	AL161988.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6728	16608	28799	3.22	1.1E+00	BFG93996.1	EST_HUMAN	60208282F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5'
7658	17508	27733	1.65	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
7715	17565	27791	4.39	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
7744	17594	27815	20.08	1.1E+00	6754021 NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA	
8033	17934	28182	2.65	1.1E+00	11057364 NT	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA	
8090	17981		3.41	1.1E+00	AF068942.1	NT	Klebsiella fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding
8447	13426		5.73	1.1E+00	8922973 NT	Homosapiens hypothetical protein FLJ11280 (FLJ11280), mRNA	
8450	18323	28581	4.41	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (ccGPDH1) mRNA, complete cds
8450	18323	28582	4.41	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (ccGPDH1) mRNA, complete cds
8662	18551	28835	4.73	1.1E+00	AF09699.1	EST_HUMAN	wf6e11x1 Scares._NFT GBC_S1 Homo sapiens cDNA clone IMAGE:2367548 3'
9300	18989		4	1.1E+00	PO7836	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
9402	19056	25310	2.13	1.1E+00	AF2216696.1	NT	Taenia solium immunogenic protein T.s76 mRNA, partial cds
9523	19570		1.54	1.1E+00	AF234169.1	NT	Dicyostelium discoideum isopentenyl pyrophosphate isomerase (Dipi) mRNA, complete cds
92	10077		3.49	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
108	10089	9904	1.14	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
412	10358		2.16	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 2S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
562	10502	20308	1.14	1.0E+00	A1251660.1	NT	Girardia tigrina mRNA for homeodomain transcription factor (so gene)
661	10595	20413	4.51	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C013
663	10597		0.95	1.0E+00	AF+25584.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1364	12692		1.04	1.0E+00	X80416.1	NT	V.carteri Algal-CAM mRNA
1722	11623	21492	1.32	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2435	12312	22208	1.4	1.0E+00	P48355	SWISSPROT	DNA GYrase SUBUNIT B
2435	12312	22209	1.4	1.0E+00	P48355	SWISSPROT	DNA GYrase SUBUNIT B

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2651	12518	22408	1.09	1.0E+00	AF131205.1	NT	Mus musculus <i>Serf1</i> protein (Serf1), survival of motor neuron protein (Smn), neuronal apoptosis inhibitory protein-rs6 (Napi-rs6), and neuronal apoptosis inhibitory protein-rs3 (Napi-rs3) genes, complete cds
2846	12774	22561	3.48	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2846	12774	22562	3.48	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2938	12865		0.99	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME I
3162	13087	22891	1.17	1.0E+00	AA628453.1	EST_HUMAN	af26g08_s1 Scares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032850 3' similar to WP:C42D8_3 CE04204 :contains element MER22 MER22 repetitive element;
3327	13247		0.81	1.0E+00	AF222761.1	NT	Rattus norvegicus neuromedin U precursor (NmU) gene, exons 5 and 6
3548	10077		1.15	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3627	13541	23328	1.44	1.0E+00	AJ23816.1	NT	Agaricus bisporus mRNA for tyrosinase
3978	13885	23660	0.86	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4178	14078		0.79	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4815	14698		0.88	1.0E+00	U75741.1	NT	Taenia ovis 45W antigen (ToW4) gene, complete cds
4951	14828		0.88	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5139	15006	24777	0.87	1.0E+00	AJ23978.1	NT	Bacillus subtilis 42.7kB DNA fragment from yvaA to yvqA
5228	15152	24919	2.49	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5568	15484	25557	4.31	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5568	15484	25558	4.31	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5719	15626	25729	4.82	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
5720	15627	25730	1.39	1.0E+00	AW4521782.1	EST_HUMAN	U1-H-B13-alk-d-08-0-U1_NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088968 3'
5908	15814	25939	2.21	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6417	16279		8.43	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14)(B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
6537	16395	26574	1.34	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
6546	16404	26583	5.99	1.0E+00	AA775191.1	EST_HUMAN	ac7gb08_s1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:888791 3'
6541	16521	26713	1.71	1.0E+00	BE86267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3548005 5'
6541	16521	26714	1.71	1.0E+00	BE86267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3548005 5'
6734	14828		1.38	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6861	16740	26932	2.7	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) [MULTIFUNCTIONAL BETA-OXIDATION PROTEIN] (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
6861	16740	26933	2.7	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) [MULTIFUNCTIONAL BETA-OXIDATION PROTEIN] (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
6967	19466			2.01	1.0E+00	BE47331.1	EST_HUMAN
7064	16941	27133	1.9	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
7339	17207	27405	1.76	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH MG_C_70 Homo sapiens cDNA clone IMAGE:3899421 5'
7460	17320	27526	1.28	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
7460	17320	27527	1.28	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
7544	17395	27607	2.03	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GKC Homo sapiens cDNA clone GKCCYA11 5'
7546	17397	27609	1.2	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida glycoprotein precursor (XZPC), mRNA, complete cds
7546	17397	27610	1.2	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida glycoprotein precursor (XZPC), mRNA, complete cds
7916	17766	28005	2.83	1.0E+00	AV758625.1	EST_HUMAN	AV758625 BM Homo sapiens cDNA clone BMFAWCD4 5'
7985	17835	28075	17.08	1.0E+00	AA004982.1	EST_HUMAN	zhs94a02.1 Scates, fetal liver, spleen,_1NFL_S, 1Homo sapiens cDNA clone IMAGE:428906 5'
7985	17835	28076	17.08	1.0E+00	AA004982.1	EST_HUMAN	zhs94a02.1 Scates, fetal liver, spleen,_1NFL_S, 1Homo sapiens cDNA clone IMAGE:428906 5'
9193	18928			2.05	1.0E+00	P75306	SWISSPROT
9513	19126			1.51	1.0E+00	AW976184.1	EST_HUMAN
9859	19350			1.67	1.0E+00	AB040980.1	NT
1553	11458	21315	0.84	9.9E-01	AF224545.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO II mRNA, complete cds
1553	11458	21316	0.84	9.9E-01	AF224545.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO II mRNA, complete cds
2598	12467	22360	0.9	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS2TC102
3553	13468			1.18	9.9E-01	AF74585.1	NT
5461	15381	25441	9.22	9.9E-01	P49657	SWISSPROT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
7336	17204			1.38	9.9E-01	U66667.1	NT
7510	17298			2.43	9.9E-01	Q28642	SWISSPROT
8097	17938	28237	2.92	9.9E-01	AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rk8
512	10454	20265	2.32	9.9E-01	P22567	SWISSPROT	AMINO ACID ACETYL TRANSFERASE (N-ACETYL GLUTAMATE SYNTHASE) (AGS) (NAGS)
3732	13644	23428	0.82	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH MG_C_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3732	13644	23430	0.82	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH MG_C_55 Homo sapiens cDNA clone IMAGE:3838461 3'
6272	16137	26292	4.61	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM993 partial groES gene for GroEL-like protein and partial groEL gene for GroEL-like protein, isolate JM983

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6272	16137	26293	4.61	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroEL-like protein, isolate JM983
8362	18239	28487	4.43	9.8E-01	BE258705.1	EST_HUMAN	6011102587F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
8362	18239	28488	4.43	9.8E-01	BE258705.1	EST_HUMAN	6011102587F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
9408	19061			9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein > we62e04x1 Soares, thymus, NHFTn Homo sapiens cDNA clone IMAGE:234594 3'
5108	14974			1.01	9.7E-01	AI660384.1	EST_HUMAN
6248	16114	26266	2.37	9.7E-01	U28716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
6952	16830	27023	1.86	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
6954	16832	27025	1.74	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
8510	18382		4.52	9.7E-01	BF511209.1	EST_HUMAN	U1-H-B14-acid-e-07-0-U1_NCI_CGAP_Subb Homo sapiens cDNA clone IMAGE:3085140 3'
9956	19419		1.39	9.7E-01	AL114281.1	NT	Baetis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4337	14234	24016	6.8	9.8E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4337	14234	24017	6.8	9.8E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4355	14251	24036	1.3	9.8E-01	AW798674.1	EST_HUMAN	PM2-UM0053-240300-005-f12 UM0053 Homo sapiens cDNA
5083	14953	24729	0.92	9.8E-01	7662375I	NT	Homo sapiens KIAA0914 gene product (KIAA0914), mRNA
5517	15435	25498	3.46	9.8E-01	Z70556.1	NT	Papovavirus B19 DNA, patient C, genome position 2448-2994
5517	15435	25499	3.46	9.8E-01	Z70556.1	NT	Papovavirus B19 DNA, patient C, genome position 2448-2994
6890	16769		1.37	9.8E-01	X952257.1	NT	P. falciparum complete gene map of plastid-like DNA (IR-A)
8808	18622	28912	4.15	9.8E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
8808	18622	28913	4.15	9.8E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
9709	19646	24989	1.52	9.8E-01	U91428.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NDH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
3715	13627	23410	1.6	9.8E-01	BE923240.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3715	13627	23411	1.6	9.8E-01	BE923240.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
7286	17143	27336	1.17	9.8E-01	AW861102.1	EST_HUMAN	RC1-CT025-241199-011-b02 CT025 Homo sapiens cDNA
3165	13090		3.37	9.8E-01	AF165990.1	NT	Bartonella claridgeiae RNA polymerase beta subunit (rpbB) gene, partial cds
3181	13106		1.67	9.8E-01	AF080985.1	NT	Pitriparinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
9354	19029		1.64	9.8E-01	BE781251.1	EST_HUMAN	601466703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868929 5'
9708	19564		1.43	9.8E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastotic leukemia viral (v-erb-b) oncogene homolog) EGFR, mRNA
1700	11601		1.11	9.8E-01	AF242382.1	NT	Homo sapiens phytanoyl-CoA hydroxylase (PHYH) gene, exon 5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2594	12464	22357		1.13	S.3E-01 BE071172.1	EST_HUMAN	RC5:BT0503-271199-011-B01_BT0503_Homo sapiens cDNA
3949	13887	23630		0.82	S.3E-01 M20219.1	NT	Bovine papillomavirus type 2, complete genome
3949	13887	23631		0.82	S.3E-01 M20219.1	NT	Bovine papillomavirus type 2, complete genome
5155	15022			1.54	S.3E-01 AF075615.1	NT	Equis caballus microsatellite LEX013
5434	15354	25410		1.62	S.3E-01 AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5482	15402	25465		3.84	S.3E-01 L36199.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
6701	16581	26771		1.88	S.3E-01 AA847040.1	EST_HUMAN	oe09b03_s1_NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357
9822	19325			1.56	S.3E-01 AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rp134 mRNA, complete cds
9954	19418			1.38	S.3E-01 U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDH-L), and Li>
3201	13125	22930		3.04	S.2E-01 BE622/02.1	EST_HUMAN	6014413871 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184'3'
5643	15556	25649		4.23	S.2E-01 BT037586.1	EST_HUMAN	601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3884661'5'
7618	17469	27638		1.38	S.2E-01	6671677 NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
7880	17740	27933		3.63	S.2E-01	11430963 NT	Homo sapiens lysosomal arylase-like protein 1 (LALP1), mRNA
7952	17802	28041		1.73	S.2E-01 BF593251.1	EST_HUMAN	7058e06_x1_NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3578219'3' similar to SW:NU5M_TRYBB
8960	18767	29059		1.85	S.2E-01 BF132402.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5'
9006	18809	29101		2.01	S.2E-01 BF680047.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018'5'
2077	11987			1.43	S.1E-01	89230561 NT	602154769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285896'5'
3169	13094	22898		0.97	S.1E-01 T26418.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
							AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
3169	13094	22899		0.97	S.1E-01 T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
4310	14207	23991		0.86	S.1E-01 U681172.1	NT	Rattus norvegicus mucin (MUC2) gene, partial cds
5919	15324	25950		2.92	S.1E-01 Q61704	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
6472	16331	26498		15.99	S.1E-01 AA806623.1	EST_HUMAN	ob71g08_s1_NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336362'3'
6551	16409	26537		2.2	S.1E-01 U72995.1	NT	Rattus norvegicus Rab33 GDP/GTP exchange protein mRNA, complete cds
9445	19641			30.05	S.1E-01 AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3170	13095	22900		0.89	S.0E-01 7661625 NT	NT	Homo sapiens DKEZP56-M2423 protein (DKEZP56-M2423), mRNA
4282	14181	23959		2.37	S.0E-01 AF098910.1	NT	Homo sapiens neuregulin III-alpha gene, partial cds
4945	14822	24589		0.82	S.0E-01 AF011729.1	NT	Oryctolagus cuniculus Rad5 (RAD5) mRNA, complete cds
6388	16230			1.45	S.0E-01 D38621.1	NT	Xenopus laevis gene for aldolase, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5494	15413	25476		2.08	8.9E-01 AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
5786	15632			1.32	8.9E-01 X60986.1	NT	Rabbit MHC Fragment RLA-DF DNA
8990	18784	29085		3.47	8.9E-01 AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
9285	18987			4.74	8.9E-01 AE002186.2	NT	Chlamydomonas pneumonae AR39, section 21 of 94 of the complete genome
4442	14336	24126		3.28	8.8E-01 O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
8430	18304	28560		2.98	8.8E-01 Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid pMA1
9108	19722			1.75	8.8E-01 D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 15/6593-17/19643
457	10401	20218		1.54	8.7E-01 AF106953.2	NT	Homo sapiens SOS1(SOS1) gene, partial cds
2353	12233	22130		1.09	8.7E-01 5901893	NT	Homo sapiens AT-binding transcription factor 1(ATBF1), mRNA
2845	12773	22560		4.64	8.7E-01 AA656833.1	EST HUMAN	nm05f11.s1 NC_ OGAP_P14.1 Homo sapiens cDNA clone IMAGE:1076877
4938	14816			2.51	8.7E-01 AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzene 1,2-dioxxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzene 1,2-dioxxygenase alpha-ISP protein OhbB (ohbB), and put>
7613	17464	27681		1.45	8.7E-01 AE004983.1	NT	Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome
8206	18090	28343		5.47	8.7E-01 BF363970.1	EST HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
8970	18776	29067		4.16	8.7E-01 BF107694.1	EST HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone MAGE-4043564 3'
8970	18776	29068		4.16	8.7E-01 BF107694.1	EST HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone MAGE-4043564 3'
9488	19534			2.78	8.7E-01 AV661898.1	EST HUMAN	AV661898 GLC Homo sapiens cDNA clone GLCGYG07 3'
466	10409			1.66	8.6E-01 XJ7012.1	NT	Rat GFI1 gene for insulin-like growth factor II
840	10787	20618		3.62	8.6E-01 W69089.1	EST HUMAN	zdi4ed3.r1 Scores_Fetal_heart_NbH-H19W Homo sapiens cDNA clone MAGE-343516 5'
2224	12109	22012		1.01	8.6E-01 4503210	NT	Homo sapiens cytochrome P-450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3568	13482	23273		0.81	8.6E-01 AL161865.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3730	13642	23427		1.29	8.6E-01 UU9724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
5595	15509	25586		11.82	8.6E-01 X60547.1	NT	Chicken lipoprotein lipase gene
5595	15509	25587		11.82	8.6E-01 X60547.1	NT	Chicken lipoprotein lipase gene
6030	15834	26065		2.14	8.6E-01 AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6030	15834	26066		2.14	8.6E-01 AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6626	16506			1.52	8.6E-01 AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
6443	16304	26469		2.75	8.5E-01 BE4261.2	EST HUMAN	60106710741 NIH_MGC_10 Homo sapiens cDNA clone MAGE-3435305 5'
7924	17774	28013		1.36	8.5E-01 AB006799.1	NT	Cyanidium caddarium gene for SigC, complete cds
7924	17774	28014		1.36	8.5E-01 AB006799.1	NT	Cyanidium caddarium gene for SigC, complete cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9430	19643			2.52	8.5E-01	11418543 NT	Homo sapiens human immunodeficiency virus type I enhancer-binding protein 1 (HIVEP1), mRNA
9436	19075			2.63	8.5E-01	9507008 NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptprn5), mRNA
9683	19238	25243		1.29	8.5E-01	AB030818.1 NT	Mus musculus mper1 gene for period1, complete cds
4108	14008	23785		0.84	8.4E-01	Af143509.1 NT	Mus musculus NK cell receptor 2B4 gene, promoter region and partial cds
5378	19443	25145		2.7	8.4E-01	L78726.1 NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5378	19443	25146		2.7	8.4E-01	L78726.1 NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7721	17571			3.13	8.4E-01	AJ248287.1 NT	Pyrococcus abyssi complete genome, segment 5/6
724	10656	20486		2.31	8.3E-01	M93437.1 NT	Thermus thermophilus cytochrome c-552 (cytcA) and CycB (cytB) genes, complete cds
3056	12983	22774		2.64	8.3E-01	AL161506.2 NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3739	13651	23434		1	8.3E-01	AB010879.1 NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
3930	13659	23619		3.11	8.3E-01	Y19177.1 NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
4917	14796	24570		1.12	8.3E-01	U46916.1 NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
4917	14796	24571		1.12	8.3E-01	U46916.1 NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
5177	14796	24570		0.95	8.3E-01	U46916.1 NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
5177	14796	24571		0.95	8.3E-01	U46916.1 NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
5222	15145	24839		2.13	8.3E-01	AL161540.2 NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
7573	17424			4.2	8.3E-01	AI791952.1 EST_HUMAN	mn0ff12.y5 NCI CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to Contains THR, tit THR repetitive element;
7822	17672	27914		1.23	8.3E-01	AF098070.1 NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
7867	17717	27962		3.1	8.3E-01	AF108133.1 NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
8062	17953	28204		2.46	8.3E-01	AE000903.1 NT	Methanobacterium thermotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
8076	17967			2.46	8.3E-01	7212472 NT	Phytophthora infestans mitochondrial, complete genome
8623	18488	28760		2.03	8.3E-01	AF020503.1 NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2006	11688	21789		2.99	8.2E-01	AB00489.1 NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2043	11934			1.51	8.2E-01	Af445589.1 NT	Mus musculus trophinin (Tm) gene, complete cds
2646	12513			1.14	8.2E-01	AW376990.1 EST_HUMAN	IL3-CT0219-161198-03-1-C08 CT0219 Homo sapiens cDNA
5045	14917	24691		1	8.2E-01	AB00489.1 NT	Rattus norvegicus mRNA for RPHO-1, complete cds
6122	16016	26154		3.26	8.2E-01	AW379433.1 EST_HUMAN	CN4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
6309	19462	26330		3.58	8.2E-01	Z12126.1 NT	S.cerevisiae METT, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and tRNA polymerase alpha (partial)
7788	17638	27871		1.53	8.2E-01	AF052659.1 NT	Homo sapiens thioredoxin-related protein mRNA, complete cds
7937	17787	28023		6.66	8.2E-01	Q9JLJ0 SWISSPROT	MCKUSICK-KAUFLMANBARDET-BIELDL SYNDROMES PUTATIVE CHAPERONIN

Table 4
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7937	17787	28029	6.66	8.2E-01	Q9AI70	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIELDI SYNDROMES PUTATIVE CHAPERONIN
8909	18717	29011	2.81	8.2E-01	L0127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
8966	18772	29064	6	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
							yw14d02.1 Soares placenta. 869 weeks. 2NbHP81g9W Homo sapiens cDNA clone IMAGE:252195 5'
8971	18777	29069	6.65	8.2E-01	I87398.1	EST_HUMAN	
9451	19053	25284	1.73	8.2E-01	AJ001261.1	NT	
2731	12593		1.29	8.1E-01	AF191639.1	NT	
3412	13329	23130	2.81	8.1E-01	AF050966.1	NT	
3412	13329	23131	2.81	8.1E-01	AF050966.1	NT	Homo sapiens MHC class 1 region
5992	15897	26020	2.49	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
5992	15897	26021	2.49	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
8775	18592	28879	1.94	8.1E-01	BEF38558.1	EST_HUMAN	RCD-TN0050-220800-025-d10 TN0080 Homo sapiens cDNA
8775	18592	28880	1.94	8.1E-01	BEF38558.1	EST_HUMAN	RCD-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
9166	18909	25343	1.84	8.1E-01	AEG01171.1	NT	Thermatoga maritima section 23 of 136 of the complete genome
170	10142		3.02	8.0E-01	A1271510.1	NT	Staphylococcus aureus partial pta gene for phosphate acyltransferase allele 15
285	10250	20070	3.76	8.0E-01	AJ132772.1	NT	Bos taurus fub and rif genes
1990	11884		1.83	8.0E-01	BF530962.1	EST_HUMAN	602072473F1 NCL CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215091 5'
3039	12967	22761	2.73	8.0E-01	AF472897.1	NT	Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds
3273	13194	22993	1.14	8.0E-01	AB006193.1	NT	Mus musculus gene for oviductal glycoprotein, complete cds
3643	13557		1.8	8.0E-01	AL162758.2	NT	Neisseria meningitidis serogroup A strain 72491 complete genome, segment 7/7
4432	14327	24115	5.65	8.0E-01	X83739.2	NT	G. gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
6661	16541		2.84	8.0E-01	AW910489.1	EST_HUMAN	RC0-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA
446	10390	20211	3.78	7.9E-01	D11476.1	NT	Lymantia dispar nucleic polyhedrosis virus gene for DNA polymerase, complete cds
693	10631		1.16	7.9E-01	AEG02130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1587	11491		65.97	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1634	11558		1.37	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2216	12102	22006	5.24	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2217	12103	22007	2.29	7.9E-01	AF130459.1	NT	Danio rerio Tp4-associated protein Tap1A (tap1A) mRNA, complete cds
3472	13388	23193	2.75	7.9E-01	AF228864.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4204	14103		0.92	7.9E-01	BE263612.1	EST_HUMAN	6019203F1 NIH MGCG 7 Homo sapiens cDNA clone IMAGE:3535785 5'
4508	14401	24188	1.02	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4508	14401	24189	1.02	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5075	14945	24720	0.84	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
5075	14945	24721	0.84	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5084	14954			1.01	7.9E-01 M29930.1	NT	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17
6721	16601	26790		2.43	7.9E-01 X80966.1	NT	P.sativum GR gene
7504	17373	27582		4.78	7.9E-01 U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
7781	17681	27864		3.95	7.9E-01 P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
8372	18249			2.36	7.9E-01 7662471 NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA	
8543	18415	28682		2.48	7.9E-01 P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
858	10784			1.75	7.8E-01 Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh041
2229	12114	22016		3.2	7.8E-01 AW939567.1	EST_HUMAN	EST371637 IMAGE sequences, MAGF Homo sapiens cDNA
4603	14491	24278		0.79	7.8E-01 U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5698	15607	25709		2.32	7.8E-01 AF15556.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds
7323	17199	27399		1.27	7.8E-01 Y10139.1	NT	D.discoideum racGAP gene
9424	19623			1.42	7.8E-01 L2920.1	NT	Arabidopsis thaliana 1-amino-1-cyclopentanecarboxylate synthase (ACS5) gene, complete cds
138	10112	19932		6.33	7.7E-01 AF184945.1	NT	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAlpha) and major histocompatibility protein class II beta chain (IIBeta) genes, complete cds; butyrophilin-like (NC9), butyrophilin->
709	10641			1.85	7.7E-01 AF050157.1	NT	
2680	12545	22436		2.8	7.7E-01 O33915	SWISSPROT	CITRATE SYNTHASE
3313	13234			0.8	7.7E-01 8393408 NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNAC-T7), mRNA	
3549	13464	23259		4.45	7.7E-01 AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4297	14195	23979		2.88	7.7E-01 AF199488.1	NT	Coturnix columnaris sub-species japonica beta-actin mRNA, partial cds
4297	14195	23980		2.88	7.7E-01 AF199488.1	NT	Coturnix columnaris sub-species japonica beta-actin mRNA, partial cds
5445	15335	25386		1.44	7.7E-01 P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5445	15335	25387		1.44	7.7E-01 P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5626	15541	25630		1.95	7.7E-01 R08600.1	EST_HUMAN	yf24b02.s1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:127755.3'
9212	10112	19932		2.6	7.7E-01 AF184945.1	NT	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
9311	19004			6.14	7.7E-01 11497621 NT	Archaeoglobus fulgidus, complete genome	
5710	15618	25720		4.04	7.6E-01 AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
5710	15618	25721		4.04	7.6E-01 AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6699	16579	26770	1.41	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (NmU) gene, partial cds; NPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
6726	16606	26796	2.04	7.6E-01	6857752	NT	Mus musculus adhillin (Adhl-pending), mRNA
6726	16606	26797	2.04	7.6E-01	6857752	NT	Mus musculus adhillin (Adhl-pending), mRNA
7184	17061	27252	1.28	7.6E-01	6753577	NT	Mus musculus cytochrome P450_2B9, phenobarbital inducible, type a (Cyp2b9), mRNA
7347	17215	27414	7.62	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
7347	17215	27415	7.52	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
8664	18553	28837	2.31	7.6E-01	X86347.1	NT	H.asperase mRNA for neurofilament NF70
8664	18553	28838	2.31	7.6E-01	X86347.1	NT	H.asperase mRNA for neurofilament NF70
8948	18756		4.81	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
9073	18850		2.74	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0885 protein, partial cds
502	10444		1.52	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21/C101
569	10508	20315	2.23	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3315	13236	23040	0.88	7.5E-01	C14203.1	EST_HUMAN	C14203 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-037E11'5'
4573	10083	19900	13.92	7.5E-01	8922672	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ_10783), mRNA
9381	19042		3.57	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSP) gene, complete cds
9828	19329	25209	1.87	7.5E-01	D90907.1	NT	Synechocystis sp. PCC6803 complete genome, 9/27..1056667..1188885
9884	19368	25190	1.42	7.5E-01	AE000823.1	NT	methanobacterium thermoaotrophicum from bases 317350 to 328792 (section 29 of 143) of the complete genome
1114	11029	20869	1.23	7.4E-01	AI598146.1	EST_HUMAN	tn14p09_x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element contains element MIR repetitive element;
2295	12477	22076	0.97	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3665	13579	23366	1.22	7.4E-01	AF112538.1	NT	Malva pusilla actin (Actl) mRNA, complete cds
4213	14111	23889	4.43	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21/C046
7253	17135	27328	7.23	7.4E-01	BE747503.1	EST_HUMAN	60/1573026/F1 NIH MGCG_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9041	18828		3.28	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
9150	18901		1.59	7.4E-01	AI472644.1	EST_HUMAN	ta13n01_x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4515	14408	24194	0.95	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4602	14490	24277	4.76	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5127	14984		1.1	7.3E-01	5360211	NT	Homo sapiens growth arrest specific 7 (GAS7), transcript variant b, mRNA
5984	15889	26010	5.61	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
5984	15889	26011	5.61	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6454 16315	26480	26480	7.42	7.3E-01	M26511.1	NT	V.alginolyticus sucrase (scrB) gene, complete cds
6454 16315	26481	26481	7.42	7.3E-01	M26511.1	NT	V.alginolyticus sucrase (scrB) gene, complete cds
8729 18585	28870	28870	3.29	7.3E-01	AA678019.1	EST_HUMAN	Z125008.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799.3'
8729 18585	28871	28871	3.29	7.3E-01	AA678019.1	EST_HUMAN	Z125008.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799.3'
814 10742			2.54	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1914 11809	21687	21687	3.68	7.2E-01	X79140.1	NT	N.tabacum NefF-4A13 mRNA
2412 12289	22186	22186	1.46	7.2E-01	AB09605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3028 12956	22748	22748	1.16	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3406 13323	23124	23124	2.14	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6/A-1 allele, complete cds
3795 13707	23494	23494	1.31	7.2E-01	BF238350.1	EST_HUMAN	602035589F1_NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183222.5'
4660 14546	24335	24335	2.41	7.2E-01	D80314.1	NT	L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5064 14934	24706	24706	1.16	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor G/HM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha 2$
5064 14934	24707	24707	1.16	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor G/HM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha 2$
6923 16801	26994	26994	1.21	7.2E-01	AF236061.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
7922 17772	28011	28011	2.22	7.2E-01	BF670061.1	EST_HUMAN	602118581F1_NIH_MGC_56 Homo sapiens cDNA clone IMAGE:42753B1.5'
8121 18009	28256	28256	4.78	7.2E-01	U822623.1	NT	Rattus norvegicus cytochrome c mRNA, complete cds
9570 19160			4.08	7.2E-01	AP00063.1	NT	Aepyprum pannix genomic DNA, section 6/7
677 10610	20431	20431	10.38	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3024 12952	22745	22745	10.8	7.1E-01	A1270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4114 14014	23793	23793	2.93	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
4114 14014	23794	23794	2.93	7.1E-01	7305360	NT	Mus musculus otogelin (Otg), mRNA
5623 15538	25625	25625	1.56	7.1E-01	BF681034.1	EST_HUMAN	602155438F1_NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344.5'
5623 15538	25626	25626	1.56	7.1E-01	BF681034.1	EST_HUMAN	602155438F1_NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344.5'
6149 16022	26162	26162	6.97	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvotetrahydropterin synthase (pt) gene, complete cds
7669 17519	27746	27746	2.25	7.1E-01	BE004405.1	EST_HUMAN	601496330F1_NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495.5'
9363 19550			1.61	7.1E-01	AA421492.1	EST_HUMAN	Z10611.s1 Soares_tests_NH Homo sapiens cDNA clone IMAGE:731109.3'
1209 11118	20966	20966	1.04	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1209 11118	20967	20967	1.04	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2399	12277	22173	1.4	7.0E-01	NG62412.1	EST_HUMAN	yZ73e07_s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
2399	12277	22174	1.4	7.0E-01	NG62412.1	EST_HUMAN	yZ73e07_s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
4989	14864		1.95	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6880	16759		8.1	7.0E-01	AE00253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
8463	18336	28599	2	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCHE04 5'
8463	18336	28600	2	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCHE04 5'
954	10878	20726	15.73	6.9E-01	U68674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
954	10878	20726	15.73	6.9E-01	U68674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1288	11196	21049	2.21	6.9E-01	AA593580.1	EST_HUMAN	mm28a09_s1 NC1_CGA_P_Gas1 Homo sapiens cDNA clone IMAGE:1085f176 3'
3182	13107	22911	1.63	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
3399	13316	23117	0.85	6.9E-01	Y17373.1	NT	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PG 2811
6652	16532	26726	2.73	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
6652	16532	26727	2.73	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8582	18450	28719	3.56	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
8582	18450	28720	3.56	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
9016	19543		2.37	6.9E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKH-14)
941	10866	20713	1.03	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2639	12506		1.16	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 34/18852-3573470
2799	11502	21362	1.58	6.8E-01	AA854475.1	EST_HUMAN	ai75a05_s1 Soares_pariathyroid tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to 9b:X56411_ma1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4469	14363	24153	1.26	6.8E-01	JD00762.1	NT	Rat(hooded) prolactin gene : exon III and flanks
4749	14634	24420	0.83	6.8E-01	4758521	NT	Homo sapiens hevin (HEVIN) mRNA
7556	17407	27622	1.52	6.8E-01	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
8437	18311	28566	2.34	6.8E-01	AJ276675.1	NT	Stagonospora avenae bglI gene for beta-glucosidase, exons 1-4
8437	18311	28567	2.34	6.8E-01	AJ276675.1	NT	Stagonospora avenae bglI gene for beta-glucosidase, exons 1-4
8453	18331	28593	2.59	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
8453	18331	28594	2.59	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
8619	18485	28757	1.79	6.8E-01	AF164151.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds

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295	10259	20080	29.34	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
336	10295	20110	19.53	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2100	11989	21887	1.57	6.7E-01	AA451864.1	EST_HUMAN	zr12g12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element ;
2120	12713	21908	3.59	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NM/DMC isoform (Nmndmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2966	12893	22692	3.7	6.7E-01	6678580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4350	11246	24032	0.96	6.7E-01	X74421.1	NT	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase
4881	14762	24538	0.85	6.7E-01	AW079110.1	EST_HUMAN	xe05g12.x1 NCL CGAP_Co17 Homo sapiens cDNA clone IMAGE:2574598 3'
5182	15046	24811	0.89	6.7E-01	AJ252942.1	NT	Dendrobium fimbriatum mRNA for phosphoenolpyruvate carboxylase, partial
5627	15542	25651	1.62	6.7E-01	AE01486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6817	15723	25686	1.42	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
5817	15723	25837	1.42	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6329	16192		3.98	6.7E-01	AE04606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
6342	16205	26367	1.46	6.7E-01	AE01486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8323	18200	28449	2.23	6.7E-01	BF35649.1	EST_HUMAN	CM3-HTT0789-010800-197-c03 H10769 Homo sapiens cDNA
8754	17903	28147	3.69	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
2452	12329	22227	0.87	6.6E-01	AF075240.1	NT	Homo sapiens SLT1 protein (SLT2), mRNA, partial cds
2987	12532	22422	1.29	6.6E-01	AF195339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3445	13362	23168	1.04	6.6E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1 like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3608	13522	23310	3.05	6.6E-01	Y07659.1	NT	C.albicans random DNA marker, 282bp
4020	13924		0.87	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rb1 gene, and sodium phosphate transporter (NPT3) gene, complete cds
56822	15728	25840	3.96	6.6E-01	6680577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
6525	16384	26363	3.63	6.6E-01	AV660506.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLCG04 3'
7571	17422		2.41	6.6E-01	AL165278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9619	19197	25256	1.35	6.6E-01	AE004382.1	NT	Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome
608	10544	20352	1.37	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
608	10544	20353	1.37	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds

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3386	13304		23104	5.1	6.5E-01 AB041225.1	NT	Mus musculus gene for Tubb2, complete cds
3951	13859	23653	1.08	6.5E-01	4504632	NT	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA
4185	14085	23860	4.17	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4215	14113	23890	0.86	6.5E-01	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
4994	14869	24632	2.27	6.5E-01	U28921.1	NT	Phasellus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5175	15041		0.88	6.5E-01	U37258.1	NT	Acetobacter xylinum putative ATP binding protein delta-AcpB gene, partial cds, and GDP-mannose:cellobiosyl-diphosphoryltransferase gene, complete cds
6036	15939	26071	1.38	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7919	17769	28008	2	6.5E-01	AF198676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
8030	17922	28168	3.24	6.5E-01	H87583.1	EST_HUMAN	yw17706.11 Soares_placenta_8to9weeks_2NbHP8toW Homo sapiens cDNA clone IMAGE:252515.5'
8073	17964	28215	4.03	6.5E-01	AA601287.1	EST_HUMAN	no15e07_s1 NCI_CGAP_Pher1 Homo sapiens cDNA clone IMAGE:1100748.3'
8170	18058		4.27	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1/007810.5'
8877	18689	28981	2.3	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
9419	19069		2.79	6.5E-01	BE465050.1	EST_HUMAN	hv74at10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130.3
9651	19490		1.69	6.5E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL097c
252	10218	20035	5.4	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3410	13327	23128	2.45	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3785	13697	23484	1.34	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4389	14285	24066	0.84	6.4E-01	Y12488.1	NT	M. musculus whn gene
4389	14285	24067	0.84	6.4E-01	Y12488.1	NT	M. musculus whn gene
7007	16884	27076	1.76	6.4E-01	AE01247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
7807	17657	27895	13.62	6.4E-01	U88282.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
7818	17668	27908	1.44	6.4E-01	BF670405.1	EST_HUMAN	602150289f1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291126.5'
9528	19135		6.34	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSCGC09.5'
9851	19553		1.65	6.4E-01	9845300	NT	Rat cytomegalovirus Maestricht, complete genome
427	10372	20196	4.41	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
524	10466	20277	2.15	6.3E-01	U32659.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2116	12005	21903	3.87	6.3E-01	U81136.1	NT	Shigella flexneri multi-antibiotic resistance locus
2534	12408	22300	3.89	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2534	12408	22301	3.89	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2983	12911		0.93	6.3E-01	Y17275.1	NT	Lycopersicon esculentum pgsa gene, complete CDS

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3985	13892	23668		1.38	6.3E-01	XK9675.1	NT
6959	16837			3.17	6.3E-01	BE902044.1	EST_HUMAN
7150	17027	27223		1.67	6.3E-01	S62927.1	NT
7421	17298	27495		2.72	6.3E-01	9627521	NT
7421	17298	27496		2.72	6.3E-01	9627521	NT
8004	17854	28095		1.4	6.3E-01	AED00313.1	NT
8413	18288	28543		2.27	6.3E-01	AA877715.1	EST_HUMAN
8647	18511	28791		11.72	6.3E-01	AI904160.1	EST_HUMAN
8725	18581	28865		1.94	6.3E-01	P47003	SWISSPROT
8868	18680	28969		1.98	6.3E-01	P36073	SWISSPROT
9128	19697	24899		9.21	6.3E-01	9910293	NT
9220	18944			1.54	6.3E-01	AF105227.1	NT
9435	19619			1.58	6.3E-01	X83528.1	NT
5578	15493	25569		2.12	6.2E-01	Q10135	SWISSPROT
6426	16287			3.06	6.2E-01	AF022253.1	NT
6831	16710	26903		5.45	6.2E-01	HT72255.1	EST_HUMAN
7435	16448	26638		1.71	6.2E-01	BE622687.1	EST_HUMAN
7476	17336			2.56	6.2E-01	M24461.1	NT
7799	17649	27886		7.14	6.2E-01	AL161511.2	NT
8007	17857	28099		5.02	6.2E-01	P27410	SWISSPROT
8007	17857	28100		5.02	6.2E-01	P27410	SWISSPROT
2345	12225			4.5	6.1E-01	6678076	NT
4931	14809	24577		0.99	6.1E-01	L20427.1	NT
4931	14809	24578		0.99	6.1E-01	L20427.1	NT
6104	15988	26134		3.78	6.1E-01	MG6473.1	NT
6104	15988	26135		3.78	6.1E-01	MG6733.1	NT
6792	16671	26863		3.72	6.1E-01	AF033535.1	NT
7108	16985	27175		1.75	6.1E-01	11431065	NT
7108	16985	27176		1.75	6.1E-01	11431065	NT
7449	17286	27492		19.47	6.1E-01	AF236117.1	NT
7449	17286	27493		19.47	6.1E-01	AF236117.1	NT

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7778	17628	27860	1.59	6.E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
486	10429	20243	0.92	6.E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
549	10490		2.64	6.E-01	5802999	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1339	11245	21103	1.76	6.E-01	AF06253.1	NT	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds
3744	13656	23438	1.02	6.E-01	AJ233996.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
5227	15151	24918	1.56	6.E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5339	15280	25086	2.58	6.E-01	AW139713.1	EST_HUMAN	U1-H-B1-aeb-a-10-0-Jls1 NCI_OGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619'3'
5940	15845	25968	2.61	6.E-01	U38813.1	NT	Musca domestica insecticide-sensitive strain voltage-sensitive sodium channel mRNA, complete cds
6350	16213	26375	6.2	6.E-01	AJ277681.1	NT	Homo sapiens partial LM01 gene for LIM domain only 1 protein, exon 1
6725	16605	26794	4.19	6.E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI-TARAZU
6725	16605	26795	4.19	6.E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI-TARAZU
7653	17503	27727	1.69	6.E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
7894	17744		1.43	6.E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)
8411	18286	28541	1.78	6.E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
8411	18286	28542	1.78	6.E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
8838	18651	28939	2.74	6.E-01	AJ420623.1	EST_HUMAN	ff08f7.X1 NCI_OGAP_Pt28 Homo sapiens cDNA clone IMAGE:2095621'3'
9500	19115	25291	1.64	6.E-01	11421663	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
9787	19554	25065	2.1	6.E-01	9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
9809	19484		2.18	6.E-01	BE1757617.1	EST_HUMAN	RC1-HT0375-03050-015-c03 HT0375 Homo sapiens cDNA
984	10907	20752	1.25	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3232	13156	22954	4.85	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21/C067
3232	13156	22955	4.85	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21/C067
4129	14029		4.12	5.9E-01	AF162756.1	NT	Rattus norvegicus cenexin 2 mRNA, partial cds
5889	15795	25917	2.1	5.9E-01	AF065440.2	NT	Homo sapiens low density/lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
8061	17952	28203	2.67	5.9E-01	Q9Y013	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
8328	18205	28454	3.1	5.9E-01	AW037175.1	EST_HUMAN	PM1-DT0041-190100-002-h03 DT0041 Homo sapiens cDNA
8529	18401	28669	2.36	5.9E-01	AF064626.1	NT	Mus spreatus strain SPRET/Ei CD48 antigen (Cd48) gene, partial cds
9165	18908	25342	1.91	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
9404	19057		2.18	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5'-phosphate decarboxylase, complete cds
9614	19193		4.15	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN [LC2]
1867	11763	21637	1.44	5.9E-01	P40472	SWISSPROT	SIM1 PROTEIN

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3902	13812	23566	0.96	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone [MAGE:407613] 5'
4413	14307	24090	2.81	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4690	14576		1.04	5.8E-01	AF110846.1	NT	Megastoma scalaris sex-luteal homolog (Megst) gene, partial cds, alternatively spliced products
5753	15561	25768	1.29	5.8E-01	D78659.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (TFujiiwara) Homo sapiens cDNA clone GEN-500E06 5'
6077	16060		2.3	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
6604	16484		2.62	5.8E-01	H41571.1	EST_HUMAN	yn91b03_s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone [MAGE:175757] 3' similar to gb:ST8187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
6764	16643	26830	2.23	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
6764	16643	26831	2.23	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
7153	17030	27224	8.64	5.8E-01	AJ20774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
8338	18235	28483	8.47	5.8E-01	AJ242213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
8396	18272		3.23	5.8E-01	BT700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone [MAGE:4284403] 5'
8482	18355		1.78	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone [MAGE:4284403] 5'
3186	13111	22915	1.48	5.7E-01	Q3WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3460	13376		2.43	5.7E-01	AB033503.1	NT	
3829	13741	23553	1.65	5.7E-01	AF011681.1	NT	Populus euramericana peats-2 mRNA for 1-amino cyclopropane-1-carboxylate synthase, complete cds
5201	15064	24827	2.24	5.7E-01	U78517.1	NT	Homo sapiens T cell receptor beta chain (BV6S7**2-BJ1S1) mRNA, partial cds
5836	15742	25854	3.72	5.7E-01	BF035413.1	EST_HUMAN	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor II (cAMP-GEFII) mRNA, partial cds
6100	15110	24874	1.41	5.7E-01	AL111440.1	NT	601454962F1 NIH_MGC_66 Homo sapiens cDNA clone [MAGE:3883850] 5'
6564	16422	26603	2.12	5.7E-01	P00373	SWISSPROT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9124	18883		1.68	5.7E-01	BE715051.1	EST_HUMAN	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
3318	13239	23043	1.21	5.6E-01	AB018283.2	NT	MR3-HT0736-180700-003-ad02 HT0736 Homo sapiens cDNA
3318	13239	23044	1.21	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3868	13720	23509	0.83	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 13
4146	14046	23818	0.83	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
7111	16688	27180	4.16	5.6E-01	AV684703.1	EST_HUMAN	AV584703 GKC Homo sapiens cDNA clone GKCFSE05 5'
7111	16688	27181	4.16	5.6E-01	AV684703.1	EST_HUMAN	AV584703 GKC Homo sapiens cDNA clone GKCFSE05 5'
9023	18817		2.46	5.6E-01	BE88280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone [MAGE:3915457] 5'
9137	18893	28794	1.73	5.6E-01	AA43535.1	EST_HUMAN	ng75gr10_s1 NCL_CGAP_Pf6 Homo sapiens cDNA clone [MAGE:940674] similar to contains element PTT77 repetitive element;
9524	19133		1.32	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
9919	19392		3.09	5.6E-01	BF579829.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone [MAGE:4271334] 5'

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1193	11103	20949	1.09	5.5E-01	8395912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2668	12533	22423	2.88	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2668	12533	22424	2.88	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P20; NUCLEOPROTEIN P10]
2888	12815	22608	1.34	5.5E-01	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (<i>S. cerevisiae</i> homolog)-like (SKIV2L), mRNA
3027	12995		1.39	5.5E-01	H46219.1	EST_HUMAN	j018ar0.51 Soares adult brain N2b5nlB55Y Homo sapiens cDNA clone IMAGE:1782663
3196	13121	22926	3.1	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3634	13548	23335	1.29	5.5E-01	P148755	SWISSPROT	FOS-RELATED ANTIGEN-1
139	10113	19933	3.74	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
139	10113	19934	3.74	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
570	10509	20316	2.61	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsa (gsta) genes, complete cds; and unknown genes
570	10509	20317	2.61	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsa (gsta) genes, complete cds; and unknown genes
1250	11157	21006	2.24	5.4E-01	AW895087.1	EST_HUMAN	QV4-NN040-070400-160-cd4 NN040 Homo sapiens cDNA
2059	11949		2.78	5.4E-01	AE002247.2	NT	Chlamydomonas pneumoniae AR39, section 74 of 94 of the complete genome
2203	12095	21993	2.23	5.4E-01	AJ276582.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
7733	17558		2.01	5.4E-01	BfF72536.1	EST_HUMAN	602076545F-1NIH MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
8427	18301	28557	2.87	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
8892	18702	28996	4.51	5.4E-01	Q606175	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSEN HEAVY CHAIN)
8892	18702	28997	4.51	5.4E-01	Q606175	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSEN HEAVY CHAIN)
9087	18862		2.12	5.4E-01	A1856398.1	EST_HUMAN	wI37g04.x1 NCI_CGAP_Ur1 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
505	10447	20260	2.02	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes; >
2093	11982	21877	0.91	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2093	11982	21878	0.91	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2755	12617	22508	8.24	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2755	12617	22509	8.24	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3205	13129	22931	2.92	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4117	14017			1.29	5.3E-01 U39687.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5350	15270	25098		1.75	5.3E-01 AI820921.1	EST_HUMAN	zu42h12_5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5360	15270	25099		1.75	5.3E-01 AI820921.1	EST_HUMAN	zu42h12_5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5467	15387	25447		1.91	5.3E-01 BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb.J02783
5467	15387	25448		1.91	5.3E-01 BE645620.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN); 7e73c12.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb.J02783
7161	17038			2.15	5.3E-01 L01950.2	NT	Prokaryotes ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
8846	18658	28946		5.62	5.3E-01 BE66291.1	EST_HUMAN	601339867.F1 NIH MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
9015	19551			2.46	5.3E-01 AA916053.1	EST_HUMAN	0350e05.s1 NCI_CGAP_B7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb.J02611
799	10728	20568		11.31	5.2E-01 L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1148	11061	20904		7.69	5.2E-01 Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)
1174	11086	20930		2.83	5.2E-01 AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
1843	11739			5.04	5.2E-01 AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C0855
2089	11988	21886		2.75	5.2E-01 AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3081	13008	22798		1.9	5.2E-01 U65942.1	NT	Chlamydophila abortus strain S26/3 POMP91A and POMP90A precursor, genes, complete cds
3199	13124			1.22	5.2E-01 D73443.1	NT	Azotobacter vinelandii fd gene for isocitrate dehydrogenase, complete cds
3359	13278			1.76	5.2E-01 AL116780.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3397	13314	23114		1.9	5.2E-01 AA984165.1	EST_HUMAN	am77g05.s1 Strategenes schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3580	13494			1.13	5.2E-01 AF020269.1	NT	Medicago sativa chloroplast; malate dehydrogenase precursor (p11mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
3582	13496	23287		1.06	5.2E-01 U823671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), cathepsin (CAT), NAD(P)H dehydrogenase-like protein (NSDH-L), and Li>
4949	14826			1.29	5.2E-01 7106444	NT	Mus musculus vanilloid receptor-like protein 1 (Vrl1), mRNA
7761	17611	27837		1.28	5.2E-01 AF43952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
9719	19290	25221		2.46	5.2E-01 AW137066.1	EST_HUMAN	U1-H-B1-acp-a-08-0-U1 s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714799 3'
9887	19370			3.43	5.2E-01 P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
601	10537	20347		1.89	5.1E-01 M55509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
632	10569	20381		3.28	5.1E-01 A1233944.1	NT	Polyangium vitellinum (strain PI vt) 16S rRNA gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
632	10569	20382	3.28	5.1E-01	A1233944.1	NT	Polyangium vitellinum (strain PI vtf) 16S rRNA gene
1632	11536		1.06	5.1E-01	X87885.1	NT	R.norvegicus mRNA for mammalian fusca protein
1977	11870		1.44	5.1E-01	BF683095.1	EST_HUMAN	602139319F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298117'5'
3984	13891	23667	3.84	5.1E-01	AI856495.1	EST_HUMAN	wf39612.x1 NCI_CGAP_UT1 Homo sapiens cDNA clone IMAGE:2427283 3'
4094	13894	23771	2.86	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
6193	15980	26116	1.57	5.1E-01	R80873.1	EST_HUMAN	yj94408.s1 Scales placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
7584	17435	27650	4.54	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
7586	17437	27653	3.57	5.1E-01	W2202.1	EST_HUMAN	65B1 Human retina cDNA Tsp509-cleaved sublibrary Homo sapiens cDNA not directional
9230	19478		3.62	5.1E-01	BF03207.1	EST_HUMAN	601556863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767'5'
9473	19100		2.03	5.1E-01	BF439982.1	EST_HUMAN	nae5110.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element;
2087	11977	21871	1.37	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2)9, mRNA
2087	11977	21872	1.37	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2)9, mRNA
2097	11986	21882	1.32	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFB), and putative chromosome replication protein (gfdA) genes, complete cds; and termination factor Rho (rho) gene>>
2097	11986	21883	1.32	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFB), and putative chromosome replication protein (gfdA) genes, complete cds; and termination factor Rho (rho) gene>>
3698	13601	23388	0.84	5.0E-01	J55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 36Sp138, partial cds
3797	13709	23495	3.44	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA11184 protein, partial cds
6961	16339		5.62	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
7442	16455	26644	3.61	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
7550	17401	27614	2.25	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
7550	17401	27615	2.25	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
7941	17791		1.27	5.0E-01	BE869218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5'
9003	18806	29099	9.32	5.0E-01	AB021490.2	NT	Oryza sativa latifolia gene for membrane glycan cyclase OIGC1, complete cds
9170	18913		2.26	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
9858	19349		2.02	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
9869	19358		2.94	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
772	10702	20541	1.98	4.9E-01	BF571462.1	EST_HUMAN	602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1864	11750	21634	1.39	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5679	15558	25688	2.46	4.9E-01	AFO20931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
5679	15558	25689	2.46	4.9E-01	AFO20931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6406	16267	26429	1.76	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7197	17074		1.41	4.9E-01	BF209791.1	EST_HUMAN	601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'
7359	19768		2.2	4.9E-01	109468863	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
9065	18846		1.43	4.9E-01	AF776912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
9851	19733		3.55	4.9E-01	AA613562.1	EST_HUMAN	ng22e11.51 NCI_CGAP_Cord10 Homo sapiens cDNA clone IMAGE:1144652 3'
4577	14136		1.12	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5381	15300	25153	8.94	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae) sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6018	15922		3.94	4.8E-01	AA659878.1	EST_HUMAN	nu85f09_s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
6330	16193		1.96	4.8E-01	5031650	NT	Homo sapiens reproduction 8 (D8S2298E) mRNA
6563	16421	26601	3.82	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6563	16421	26602	3.82	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6613	16493	26679	1.16	4.8E-01	AL1820744.1	EST_HUMAN	Y77110.5 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MER6 repetitive element;
8111	18001		2.04	4.8E-01	X83502.1	NT	S.cerevisiae ORFs from chromosome X
9369	19511		2.52	4.8E-01	AF227555.1	NT	Trypanosoma cruzi transposon VPI II SIRE repeat region
9870	19359		2.26	4.8E-01	BE790632.1	EST_HUMAN	601584324F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936909 5'
5925	15830	25953	8.36	4.7E-01	BF217173.1	EST_HUMAN	601883580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:40963387 5'
8221	1803		5.77	4.7E-01	AF102673.1	NT	Influenza A virus isolate h5N1697 hemagglutinin (HA) gene, partial cds
8434	18308	28564	2.06	4.7E-01	U41069.1	NT	Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 16, and partial cds
8682	18570	28853	2.43	4.7E-01	AW886448.1	EST_HUMAN	RC6-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
9390	19049		1.36	4.7E-01	AW341561.1	EST_HUMAN	hd11cd08_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909198 3'
3674	13558	23375	1.27	4.6E-01	AW818638.1	EST_HUMAN	RC1-ST0278-040400-018-h016 ST0278 Homo sapiens cDNA
3683	13597	23383	1.28	4.6E-01	BFG9330.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3683	13597	23384	1.28	4.6E-01	BFG9330.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5087	14957		0.97	4.6E-01	M11267.1	NT	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds
5360	15290	25111	3.38	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5360	15290	25112	3.38	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5404	15323	25372	1.78	4.6E-01	BE734781.1	EST_HUMAN	60156875F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5414 15334	25384	25384	3.29	4.6E-01	A1247679.1	EST_HUMAN	qtl59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:18490113' similar to TR:O15338 BUTYROPHILIN.
5414 15334	25385	25385	3.29	4.6E-01	A1247679.1	EST_HUMAN	qtl59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:18490113' similar to TR:O15338 BUTYROPHILIN.
5418 15339	25393	25393	1.58	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
6057 16040	26181	26181	1.47	4.6E-01	U62332.1	NT	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6057 16040	26182	26182	1.47	4.6E-01	U62332.1	NT	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6843 16722	26916	26916	13.48	4.6E-01	Bf697899.1	EST_HUMAN	602130953FI1 NIH_MGC_C_56 Homo sapiens cDNA clone IMAGE:4287828 5'
7363 17230	27430	27430	26.48	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
7363 17230	27431	27431	26.48	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
7730 17560	27802	27802	1.33	4.6E-01	A1915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
7730 17560	27803	27803	1.33	4.6E-01	A1915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
8359 18236			2.86	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (V1)
8363 18245	28495	28495	4.78	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT730-100500-07-905 HT0730 Homo sapiens cDNA
8363 18245	28496	28496	4.78	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT730-100500-07-905 HT0730 Homo sapiens cDNA
8766 17915	28160	28160	5.45	4.6E-01	AFO19369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
8766 17915	28161	28161	5.45	4.6E-01	AFO19369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
9313 19005			1.43	4.6E-01	D53316.1	EST_HUMAN	HUM105F03B Clontech human fetal brain polyA+ mRNA (#65335) Homo sapiens cDNA clone GEN-10SF03 5'
9973 19491			2.21	4.6E-01	AF120134.1	NT	Linanthus jamaicensis matrase (matR) gene, chloroplast gene encoding chloroplast protein, partial cds
1869 11765	21639	21639	1.73	4.5E-01	AEO01931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1869 11765	21640	21640	1.73	4.5E-01	AEO01931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2841 12759	22558	22558	4.87	4.5E-01	AAB7086.1	EST_HUMAN	z155a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3275 13196	22996	22996	3.97	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERI ECAN) (PLC)
3331 13251	23056	23056	1.05	4.5E-01	AFA126378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
3942 13850			1.41	4.5E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN
3982 13889	23665	23665	1.1	4.5E-01	AJ708908.1	EST_HUMAN	ass6ed9.x1 Barsleid aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
4085 15019			4.02	4.5E-01	AW873495.1	EST_HUMAN	ho60g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4862	14742	24522	0.94	4.5E-01	BE063445.2	EST_HUMAN	601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
5406	15325	25375	1.45	4.5E-01	AW608814.1	EST_HUMAN	QV2-PT0012-140/100-031-c09 PT0012 Homo sapiens cDNA
5983	15898		1.47	4.5E-01	Q00956	SWISSPROT	COAT PROTEIN
6488	16346	26515	2.49	4.5E-01	AI858849.1	EST_HUMAN	w32e02.x1 NCI_CGAP_B11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
6897	16776	26970	3.14	4.5E-01	AI64596.1	EST_HUMAN	t26g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2392644 3'
7100	16977		1.54	4.5E-01	11444786	NT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
7991	17841	28082	25.09	4.5E-01	M8606.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBCY17
7991	17841	28083	25.09	4.5E-01	M8606.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBCY17
8237	18117	28369	2.42	4.5E-01	AW591271.1	EST_HUMAN	x014h01.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
9036	19724		2.25	4.5E-01	BE871461.1	EST_HUMAN	Q64232 VIRAL INTEGRATION SITE PROTEIN INT-6, [1];
9694	19245		1.44	4.5E-01	BF337531.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
9763	19283		2.15	4.5E-01	11422099	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
9974	19632	24987	1.83	4.5E-01	AF238234.2	NT	Entamoeba histolytica diaphanous protein (dia) gene, partial cds
1991	11885		2.47	4.4E-01	6680503	NT	Mus musculus integral membrane-associated protein 1 (imap1), mRNA
2340	12220	22118	3.59	4.4E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3274	13195	22994	0.99	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3274	13195	22995	0.99	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3277	13198	22998	1.87	4.4E-01	BF056726.1	EST_HUMAN	791d02.y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
4141	14041		1.33	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605393 5'
4924	14803		0.93	4.4E-01	BE141396.1	EST_HUMAN	MRC-HTO078-131299-007-g05 HT0078 Homo sapiens cDNA
5326	15246	25050	1.99	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5326	15246	25051	1.99	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5490	15409	25474	1.3	4.4E-01	S65019.1	NT	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 360 nt]
5499	15418	25481	1.98	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5'
5624	15539	25627	1.6	4.4E-01	A1198413.1	EST_HUMAN	qf82h11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
5624	15539	25628	1.6	4.4E-01	A1198413.1	EST_HUMAN	UNKNOWN PROTEIN;
5782	15688	25798	1.79	4.4E-01	AW080795.1	EST_HUMAN	qf82h11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6582	16462		10.84	4.4E-01	Z11679.1	NT	ALATOXIN B1-ALDEHYDE REDUCTASE; S.tuberous mRNA for induced stolon tip protein (partial)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7354	17222	27422		1.29	4.4E-01 O62836	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
7723	17573	27798		1.99	4.4E-01 AI268650.1	EST_HUMAN	q639f09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
7724	17574			2.45	4.4E-01 P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
7813	17663	27903		4.67	4.4E-01 P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
7935	17785	28025		1.33	4.4E-01 S76404.1	NT	beta-HKA=H-K-ATPase beta-subunit [rat, Genomic, segment 2 of 2]
7935	17785	28026		1.33	4.4E-01 S76404.1	NT	beta-HKA=H-K-ATPase beta-subunit [rat, Genomic, segment 2 of 2]
9296	18996	25329		2.29	4.4E-01 6677874	NT	Mus musculus sodium channel, type γ , alpha polypeptide [Scn10a], mRNA
9308	19663			3.29	4.4E-01 AL163282.2	NT	Homo sapiens chromosome 21, segment HS21C08s2
9731	19267	25224		5.34	4.4E-01 9627742	NT	Autographa californica nucleopolyhedrovirus, complete genome
9824	19326			1.75	4.4E-01 P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG A (HHR23A)
405	10351	20178		1.98	4.3E-01 AF155218.1	NT	Callithrix jacchus MW/LW opsins gene, upstream flanking region
405	10351	20179		1.98	4.3E-01 AF155218.1	NT	Callithrix jacchus MW/LW opsins gene, upstream flanking region
1585	11489	21350		1.1	4.3E-01 AW865550.1	EST_HUMAN	QV4-SN0024-20040-183-601 SN0024 Homo sapiens cDNA
2843	12771			0.96	4.3E-01 AW865269.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3022	12850	22742		0.93	4.3E-01 AW869477.1	EST_HUMAN	MR0-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
3221	13145			1.53	4.3E-01 AE000698.1	NT	Aquifex aeolicus section 30 of 109 of the complete genome
4059	13981	23737		1.15	4.3E-01 J00306.1	NT	Human somatostatin 1 gene and flanks
4306	10351	20178		1.02	4.3E-01 AF155218.1	NT	Callithrix jacchus MW/LW opsins gene, upstream flanking region
4306	10351	20179		1.02	4.3E-01 AF155218.1	NT	Callithrix jacchus MW/LW opsins gene, upstream flanking region
4875	14755			1.11	4.3E-01 AL163052.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5059	14929			1.06	4.3E-01 9635250	NT	Xestia c-nigrum granulovirus, complete genome
5600	15514	25592		3.04	4.3E-01 AF179625.1	NT	Salmarit schreus olfactory receptor (SSC1186) gene, partial cds
6029	15633	26064		3.86	4.3E-01 A001678.1	NT	Coturnix coturnix japonica ifnG gene
6102	15996			4.01	4.3E-01 Q33367	SWISSPROT	DNA GYRASE SUBUNIT B
6393	16255			2.54	4.3E-01 BF348001.1	EST_HUMAN	602023134F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158296 5'
6909	16787			2.83	4.3E-01 U97040.1	NT	Methanococcus voltae flagella-related protein C1 (flac-C-fla) genes, complete cds
7608	17459	27674		1.65	4.3E-01 AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5
7608	17459	27675		1.65	4.3E-01 AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5
7872	17722	27967		1.27	4.3E-01 AW1170559.1	EST_HUMAN	xn63e05.x1 Scores_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to LEX027
8302	16049	26195		2.64	4.3E-01 AF075629.1	NT	Equis caballus microsatellite LEX027
8537	18409	28673		1.98	4.3E-01 AW939658.1	EST_HUMAN	RC3-BN0034-280200-013-c12 BN0034 Homo sapiens cDNA
8537	18409	28674		1.98	4.3E-01 AW938658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
9916	19390			2.02	4.3E-01 A0030322.1	NT	Streptomyces coelicolor whtH gene

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1335	12691	21099	1.04	4.2E-01	Q36102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
1904	11800		0.89	4.2E-01	AA761653.1	EST_HUMAN	nt224a09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288596 3'
3558	13472	23263	4.78	4.2E-01	AE003947.1	NT	Xylella fastidiosa, section 93 of 229 of the complete genome
3585	13499	23288	1.09	4.2E-01	AI286338.1	EST_HUMAN	qj94b01.x1 Soares_NhMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3803	13715	23503	0.96	4.2E-01	AW835527.1	EST_HUMAN	QV0-LT0015-180200-127-n01 LT0015 Homo sapiens cDNA
3900	13810	23595	1	4.2E-01	Q04886	SWISSPROT	SOX-8 PROTEIN
4545	14488		3.63	4.2E-01	BE073574.1	EST_HUMAN	RC5-BT0559-020300-013-E06 BT0559 Homo sapiens cDNA
4599	14487	24273	4.96	4.2E-01	AA534093.1	EST_HUMAN	ntj9h01.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4671	14557	24350	3.13	4.2E-01	R13467.1	EST_HUMAN	yf77e01.r1 Soares_infant brain 1NIH_Homo sapiens cDNA clone IMAGE:28278 5'
5503	15422	25484	1.5	4.2E-01	BF242055.1	EST_HUMAN	601879721F1NIH_MGC_55 Homo sapiens cDNA clone IMAGE:14108493 5'
5533	15450	25518	1.56	4.2E-01	AW854162.1	EST_HUMAN	RC3-CT0254-06040-029-g04 CT0254 Homo sapiens cDNA
6151	16024	26164	9.1	4.2E-01	AU58472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2004/70 3'
6151	16024	26165	9.1	4.2E-01	AU58472.1	EST_HUMAN	AU158472 PLACE22 Homo sapiens cDNA clone PLACE2004/70 3'
6184	19461	26219	2.1	4.2E-01	S82504.1	NT	Bica1-breast cancer gene rats, WF_spleen, Genomic, 419 nt, segment 2 of 2]
6217	16083	26233	5.91	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
6663	16543	26739	2.1	4.2E-01	AW957448.1	EST_HUMAN	EST3694/13 MAGE Resequences, MAGE_Homo sapiens cDNA
6663	16543	26740	2.1	4.2E-01	AW957448.1	EST_HUMAN	EST3694/13 MAGE Resequences, MAGE_Homo sapiens cDNA
6776	16655	26844	1.19	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit Vc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
7992	17842	28084	1.48	4.2E-01	AW853666.1	EST_HUMAN	MR3-SN010-280300-103-h07 SN010 Homo sapiens cDNA
8400	18276	28528	2.2	4.2E-01	AB023489.1	NT	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
8699	18517	28799	2.04	4.2E-01	BE966485.2	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
9863	19353		1.66	4.2E-01	AV731815.1	EST_HUMAN	AV731815 HTF_Homo sapiens cDNA clone HTFBH105 5'
1078	10994	20835	1.88	4.1E-01	AI905481.1	EST_HUMAN	RC-BT091-210198-142 BT091 Homo sapiens cDNA
1087	11003	20844	2.4	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB_Homo sapiens cDNA clone ADBA1ff08 5'
1087	11003	20845	2.4	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB_Homo sapiens cDNA clone ADBA1ff08 5'
1592	11496	21356	1.03	4.1E-01	AI905949.1	EST_HUMAN	PM-BT103-270498-694 BT103 Homo sapiens cDNA
2678	12543	22434	1.52	4.1E-01	7705283	NT	Homo sapiens araphinase-promoting complex subunit 7 (APC7), mRNA
2910	12686	22633	1.76	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2910	12686	22634	1.76	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3263	13186	22985	1.13	4.1E-01	AA806344.1	EST_HUMAN	oj94b08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
4177	14077	23852	2.59	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD5 IsoG, isoH, isoI, isoA, isoB, isoC, isoD, isoE and isoF genes
4203	14107		1.07	4.1E-01	AA809257.1	EST_HUMAN	om3302.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4373	14269			0.83	4.1E-01 R41726.1	EST_HUMAN	yg11b03.s1 Soares infant brain NIH Homo sapiens cDNA clone IMAGE:318143'
4567	14459	24247		1.26	4.1E-01 AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
5185	15049			0.87	4.1E-01 Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21); from 39e99281 to 4214874
5644	15557	25650		4.13	4.1E-01 BFG81993.1	EST_HUMAN	602156690F1 NIH_MGC_C_83 Homo sapiens cDNA clone IMAGE:4297319 5'
6395	16257	26418		2.91	4.1E-01 UG7535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
6683	16563	28757		1.3	4.1E-01 BFF74604.1	EST_HUMAN	602133261F1 NIH_MGC_C_81 Homo sapiens cDNA clone IMAGE:4298238 5'
7253	17130	27323		1.23	4.1E-01 6755521	NT	<i>Mus musculus</i> signaling intermediate in Toll pathway-evolutionarily conserved (Sipeo-pending), mRNA
7888	17738			1.3	4.1E-01 AL139076.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 3/6
8018	17888			1.58	4.1E-01 BFF349382.1	EST_HUMAN	CM2-HT0137-200999-010-e08 HT0137 Homo sapiens cDNA
8213	18097	28349		164	4.1E-01 X38700.1	NT	Zea mays ZMPMS2 gene for 19 kDa zein protein
8696	17880	28121		2.79	4.1E-01 Q105470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK) (HUK1)
9624	19702			1.72	4.1E-01 D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1023	10940	20783		1.27	4.0E-01 8404656	NT	Leagueus tubellus mitochondrion, complete genome
1316	11223	21079		0.96	4.0E-01 AF203478.1	NT	Drosophila melanogaster Dalmatian (dnt) mRNA, complete cds
1469	11374			4.06	4.0E-01 6679258	NT	<i>Mus musculus</i> platelet derived growth factor receptor, beta polypeptide (Pdgfb), mRNA
1960	12709	21742		1.17	4.0E-01 Z96933.1	NT	Ascocholus immersus mascot2 gene
1960	12709	21743		1.17	4.0E-01 Z96933.1	NT	Ascocholus immersus mascot2 gene
2774	10110	19931		1.09	4.0E-01 6678490	NT	<i>Mus musculus</i> ubiquitin-protein ligase e3 component n-recognition (Ubr1), mRNA
2839	12866	22665		2.24	4.0E-01 AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C0080
2939	12866	22666		2.24	4.0E-01 AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C0080
							Streptococcus pneumoniae YIC (yIC), YID (yID), penicillin-binding protein 2x (ppb2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3637	13551	23339		1.61	4.0E-01 AF068903.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRD12), exon 1
3755	13668	23451		3.24	4.0E-01 A127751.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRD12), exon 1
3755	13668	23452		3.24	4.0E-01 A127751.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRD12), exon 1
4712	14598			7.34	4.0E-01 Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
5603	15517	25596		1.31	4.0E-01 AW970610.1	EST_HUMAN	EST36261 IMAGE sequences, MAGK Homo sapiens cDNA
8959	18766			3.24	4.0E-01 L76030.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
9312	19557			2.22	4.0E-01 AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9825	19327			1.33	4.0E-01 P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN G1N2-STE3 INTERGENIC REGION
9910	19387			1.4	4.0E-01 AL139075.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 2/6
227	10196	20007		1.59	3.9E-01 AW352188.1	EST_HUMAN	CM4-HT0136-50989-014-09 HT0136 Homo sapiens cDNA
1356	11262	21119		2.1	3.9E-01 AF206618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2605	12473	22367	3.54	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1983 protein, partial cds
2673	12538	22427	5.98	3.9E-01	X820332.1	NT	H.sapiens_B-myp gene
2673	12538	22428	5.98	3.9E-01	X820332.1	NT	H.sapiens_B-myp gene
3058	12985	22776	3.63	3.9E-01	A1225896.1	NT	Sinorhizobium meliloti egl, syrB2, cyrA3 genes and ofr3
3988	13895	23672	1.47	3.9E-01	BFF92611.1	EST_HUMAN	761601_x1_NCL_CGAP_Br16_Homo sapiens cDNA clone IMAGE:3339169 3'
4919	14798	24572	1.48	3.9E-01	BE728667.1	EST_HUMAN	601563948F1 NIH_MGC_20_Homo sapiens cDNA clone IMAGE:3833699 5'
5613	15528	25611	3.53	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC_53_Homo sapiens cDNA clone IMAGE:4082055 5'
7324	17200	27400	1.5	3.9E-01	AW1958888.1	EST_HUMAN	xn86dd04_x1 Soares_NFL_T_GBC_ST_Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:094821
7503	17372	27581	1.4	3.9E-01	A1937337.1	EST_HUMAN	wp76a02_x1 NCL_CGAP_Bm25_Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW:RF45_HUMAN_P438382 BINDING REGULATOR FACTOR ;
7680	17530	27755	2.97	3.9E-01	M19879.1	NT	Human clatbindin 27 gene, exons 10 and 11, and L1 and Alu repeats
8195	18050		2.22	3.9E-01	AV695974.1	EST_HUMAN	AV695974 GKC_Homo sapiens cDNA clone GKCB1QC11 5'
9091	19642		2.49	3.9E-01	AT304554.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
9209	18940		2.38	3.9E-01	Q61670	SWISSPROT	HOMEobox PROTEIN_H_XI
9288	18980	25323	1.26	3.9E-01	AE001871.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
154	10128		7.44	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1827	11724		1.22	3.8E-01	AE003870.1	NT	Xylella fastidiosa, section 16 of 229 of the complete genome
2524	12398	22289	2.44	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myb-like transcription factor (MYB3R-3) mRNA, complete cds
2591	12726	22352	4.41	3.8E-01	6678002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
2972	12899		0.92	3.8E-01	A1251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 38SE-MP1213)
3010	12938	22732	2	3.8E-01	AF043383.1	NT	Pleuroectes americanus aminopeptidase N (ampN) gene, partial cds
3438	13355	23160	7.77	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3494	13410		0.79	3.8E-01	AI807219.1	EST_HUMAN	wf38b12_x1 Soares_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:2357855 3'
3506	13410		0.91	3.8E-01	AI807219.1	EST_HUMAN	wf38b12_x1 Soares_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:2357855 3'
3841	13752	23545	0.85	3.8E-01	6754095	NT	Mus musculus general transcription factor II (Gtf2), mRNA
5046	14918	24692	0.98	3.8E-01	BEE44653.1	EST_HUMAN	601074110F1 NIH_MGC_12_Homo sapiens cDNA clone IMAGE:3460154 5'
5445	15366	25422	1.62	3.8E-01	Q14888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
5994	15899	28023	4.47	3.8E-01	BEO7289.1	EST_HUMAN	QV3-BT0537-27/299-049-e02 BT0537_Homo sapiens cDNA clone IMAGE:2047917 3' similar to ta54f11_x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:3460154 5'
6053	16036	26177	3.81	3.8E-01	AI374601.1	EST_HUMAN	contains Alu repetitive element;
6438	16249		4.83	3.8E-01	X61597.1	NT	M.musculus gene for kallikrein-binding protein
6980	16857	27052	3.07	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7516	17304			4.11	3.8E-01 T95413.1	EST_HUMAN	ye33h6.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120589 5' similar to contains Alu repetitive element;contains PTR5 repetitive element;
8820	18653			2.82	3.8E-01 BE719219.1	EST_HUMAN	RC0-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
8939	18747	29041		2.57	3.8E-01 R42550.1	EST_HUMAN	yf92n11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
8939	18747	29042		2.57	3.8E-01 R42550.1	EST_HUMAN	yf92n11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
9297	18897			2.38	3.8E-01 AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
9422	19661			1.34	3.8E-01 U94788.1	NT	Human p53 (TP53) gene, complete cds
9530	19137			2.21	3.8E-01 BE829236.1	EST_HUMAN	QV3-ET0063-19070-271-a05 ET0063 Homo sapiens cDNA
9917	19638			1.84	3.8E-01 AF291483.1	NT	Mus musculus vomeronasal receptor VR44 (VR44) gene, complete cds
9921	19675	24993		1.37	3.8E-01 T54787.1	EST_HUMAN	yb12b11.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:73821 3' similar to gb:A06977 SERUM ALBUMIN PRECURSOR (HUMAN)
9937	19406	25180		1.3	3.8E-01 AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
9970	19420	25151		1.33	3.8E-01 AA776820.1	EST_HUMAN	an37b01.s1 Soares testis NHT Homo sapiens cDNA clone 1291657 3' similar to TR:Q15288 Q15288 NO DISTINCTIVE PROTEIN MOTIFS. ;
2431	12308	22203		9.85	3.7E-01 AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3414	13331	23133		9.48	3.7E-01 AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
4136	14036	23812		6.63	3.7E-01 AI218707.1	EST_HUMAN	ok39c07.x1 Soares NSF_F8_9W_OT PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4225	14123	23893		1.53	3.7E-01 AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4292	14190	23974		3.32	3.7E-01 AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
6235	16101	26250		2.73	3.7E-01 11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6392	16254	26415		4.51	3.7E-01 BE873743.1	EST_HUMAN	601483587F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
6392	16254	26416		4.51	3.7E-01 BE873743.1	EST_HUMAN	601483587F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
6848	16727	26921		2.34	3.7E-01 11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12orf4), mRNA
6848	16727	26922		2.34	3.7E-01 11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12orf4), mRNA
7307	17183			1.46	3.7E-01 A1271386.1	EST_HUMAN	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
7864	17714	27958		3.93	3.7E-01 A1336411.1	EST_HUMAN	q446b07.x1 Soares fetal lung Nb-H19W Homo sapiens cDNA clone IMAGE:1950997 3'
8232	18113	28365		1.81	3.7E-01 X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
8392	18288	28518		2.66	3.7E-01 A1297557.1	NT	Homo sapiens partial LIMD1 gene for LM domains containing protein 1 and KIAA0851 gene
8392	18288	28519		2.66	3.7E-01 A1297557.1	NT	Homo sapiens partial LIMD1 gene for LM domains containing protein 1 and KIAA0851 gene
8762	17911	28155		4.23	3.7E-01 X041122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
8979	18784			2.76	3.7E-01 6677678	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
9008	19303			1.87	3.7E-01 J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
9176	18917			1.94	3.7E-01 A1243325.1	NT	Chlamydophila psittaci partial omp1 gene for outer membrane protein 1
9272	18976			2.41	3.7E-01 D86976.1	NT	Human mRNA for KIAA0223 gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9634	19206			2.18	3.7E-01 AL121154.1	EST_HUMAN	DKFZp762k075_r1 762 (synonym: mmel2) Homo sapiens cDNA clone DKFZp762k075 5'
9701	19251	25217		1.52	3.7E-01 Y18000.1	NT	Homo sapiens NF2 gene
9964	19746			1.31	3.7E-01 A1237934.1	NT	Bos taurus partial statB3 gene, exons 2-15 and joined CDS
979	10902			7.17	3.6E-01 U89241.1	NT	Human mlpb gene, partial cds
1292	11199	21054		2.59	3.6E-01 T80255.1	EST_HUMAN	yd03ee05_r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443_5'
1292	11199	21055		2.59	3.6E-01 T80255.1	EST_HUMAN	yd03ee05_r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443_5'
1874	11770	21645		6.05	3.6E-01 AW580184.1	EST_HUMAN	hg33f02_x1 NCI_CGAP_GCG Homo sapiens cDNA clone IMAGE:2947419_3'
1874	11770	21646		6.05	3.6E-01 AW580184.1	EST_HUMAN	hg33f02_x1 NCI_CGAP_GCG Homo sapiens cDNA clone IMAGE:2947419_3'
1908	11803	21682		6.18	3.6E-01 AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2007	11889			1.08	3.6E-01 AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2223	12108			1.04	3.6E-01 AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2341	12221			2.39	3.6E-01 X76725.1	NT	P_irregular (P3804) gene for actin
2437	12314	22211		1.63	3.6E-01 AW872033.1	EST_HUMAN	RC5-ST071-181099-011-907 ST0711 Homo sapiens cDNA
							PROTEIN-L-SOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-SOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2589	12460	22350		2.28	3.6E-01 P242D6	SWISSPROT	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds
2889	15077			8.9	3.6E-01 AF199485.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
3424	13341	23145		1.85	3.6E-01 X76758.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
3424	13341	23146		1.85	3.6E-01 X76758.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
4308	14205	23988		1.16	3.6E-01 BE707983.1	EST_HUMAN	RC1-HT0545-150800-014-b12 HT0545 Homo sapiens cDNA
4635	14523	24312		0.85	3.6E-01 A1009608.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
4684	14570	24367		1.23	3.6E-01 A1229237.1	NT	Bacteria from anoxic bulk soil 16S rRNA gene (strain XB45)
4941	14819	24587		2.01	3.6E-01 AW389393.1	EST_HUMAN	ha02cg04_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:28725663'
5889	15805	25928		1.6	3.6E-01 Y10196.1	NT	Homo sapiens PHEX gene
6238	16104			5.49	3.6E-01 R34090.1	EST_HUMAN	yf74406_r1 Soares fetal liver spleen 1NF1_S Homo sapiens cDNA clone IMAGE:275987 5'
6317	16180	26340		1.66	3.6E-01 AW2027174.1	EST_HUMAN	wt72c10_x1 Soares_thymus_NHFTn_Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR_O16117 O15i17 FYN BINDING PROTEIN. [1]; Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
6816	16695	26886		13.42	3.6E-01 AL161583.2	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7205	17082	27269		3.37	3.6E-01	4504956 NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7205	17082	27270		3.37	3.6E-01	4504956 NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7302	17178	27380		1.4	3.6E-01 AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
7674	17524	27750		15.34	3.6E-01 Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8314	18191	28440	1.94	3.6E-01	BEE02980.1	EST_HUMAN	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
8453	18326	28585	3.69	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
8741	17890	28134	3.56	3.6E-01	AE000856.1	NT	Methanobacterium thermautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
9044	19761		1.81	3.6E-01	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
9127	18886		3.05	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
9281	18983		3.03	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
9889	19704		1.58	3.6E-01	AW190229.1	EST_HUMAN	xl60e11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
202	10174	19930	2.18	3.5E-01	6678933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
662	10596	20414	0.97	3.5E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
708	10640	20466	1.24	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
708	10640	20467	1.24	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
763	10594	20531	3.17	3.5E-01	BF129796.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1603	11508	21370	1.17	3.5E-01	BT310688.1	EST_HUMAN	601894653F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1622	11526	21384	1.05	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2563	12725	22327	1.85	3.5E-01	AA223252.1	EST_HUMAN	z108a09 s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:950872 3'
2672	12537		0.86	3.5E-01	U05897.1	NT	Fibrobacter succinogenes S85 endoglucanase E (celE) and endoglucanase D (celD) gene, complete cds
4165	14065	23839	1.92	3.5E-01	Af071253.1	NT	Danio rerio homeobox protein (hoxb5) gene, complete cds
4379	14275	24056	1.29	3.5E-01	BE146585.1	EST_HUMAN	RC5-HT0218-18-181099-011-q02 HT0218 Homo sapiens cDNA
4790	14675	24462	0.84	3.5E-01	N81203.1	EST_HUMAN	7881E1 fetal brain cDNA Homo sapiens cDNA clone 7881E1-K similar to R0789_Z40498
4849	14730	24513	3.84	3.5E-01	MI18349.1	NT	Rat leukocyte common antigen (L-CyA) gene, exons 1 through 5
6199	15959		3.47	3.5E-01	XKB505.1	NT	S.scofa mRNA for CD31 protein (PECAM-1).
6704	16584		1.88	3.5E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
7171	17048	27238	3.21	3.5E-01	4507610	NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
7612	17463	27680	1.51	3.5E-01	Q02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BII)
7688	17538	27764	5	3.5E-01	Z26825.1	NT	X.laevis gene for albumin including 5'-P enhancer
8116	18005	28251	2.99	3.5E-01	X61084.1	NT	C.griseus rhodopsin gene for opsin protein
8386	18263	28513	2.34	3.5E-01	A1243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
8386	18263	28514	2.34	3.5E-01	A1243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8951	18758	29052	3.34	3.5E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
9206	18937		2.12	3.5E-01	X64565.1	NT	B.taurus atpA1 gene for F(0)F(1)-ATP synthase alpha-subunit
9941	19616	24999	2.25	3.5E-01	H80814.1	EST_HUMAN	ys64f1.1r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597' 5'
9941	19616	25000	2.25	3.5E-01	H80814.1	EST_HUMAN	ys64f1.1r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597' 5'
691	10624		1.9	3.4E-01	A1242956.1	NT	Homo sapiens partial Nmyc (exon 3), HPV45 L2, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from C4 cervical carcinoma cell line
960	10983	20731	4.53	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, colS genes, of r222 and partial inaA gene
1304	11211	21066	1.73	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2352	12232	22129	2.81	3.4E-01	D80909.1	NT	Synechocystis sp. PCC6803 complete genome, 1/1/27, 1311235-1430418
2642	12509	22400	1.46	3.4E-01	AL161516.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28
2971	12898	22697	0.81	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2971	12898	22698	0.81	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3124	13049	22846	5.41	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3488	13404	23209	3.48	3.4E-01	AF106835.1	NT	Methylococcus sp. strain SS1 putative GrpE (grpE), DnaK (dnak), and putative DnaJ (dnaj) genes, complete cds
3722	13634		2.33	3.4E-01	BF449010.1	EST_HUMAN	7n84a01_x1_NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232' similar to TR:Q9UJ15
3965	13872		1.16	3.4E-01	AAE84196.1	EST_HUMAN	Q9UJ15_DJ18C9.1 ;
4394	14290	24074	0.78	3.4E-01	AF16341.1	NT	not1b10_s1_NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347' 3'
4544	14437	24221	1.82	3.4E-01	BE068912.1	EST_HUMAN	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4828	14710	24494	0.93	3.4E-01	BE463761.1	EST_HUMAN	MR4-BT0403-230200-202-c01_BT0403 Homo sapiens cDNA
4870	14750		3.57	3.4E-01	AI240973.1	EST_HUMAN	hy17d09_x1_NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3197585' 3' similar to contains L1.13 L1 repetitive element;
4970	14845	24614	1.2	3.4E-01	X16544.1	NT	q95c05_x1_NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208' 3' similar to contains Alu repetitive element;
5487	15406	25468	2.85	3.4E-01	AL161594.2	NT	Sea urchin nsP70 gene II for heat shock protein 70
5551	15467		4.71	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5654	15566		2.06	3.4E-01	L02971.1	NT	zr12dt1_s1 Stratagene hNT neuron (4537233) Homo sapiens cDNA clone IMAGE:547221' 3'
5715	15623	25724	2.57	3.4E-01	AW204505.1	EST_HUMAN	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3D proteins RNA, complete mature peptides and cds
5780	15687	25796	1.47	3.4E-01	AL120544.1	EST_HUMAN	Ui-H-B1'-acie-12-0-U1.s1_NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582' 3'
6045	15948		1.52	3.4E-01	N95225.1	EST_HUMAN	DKFZp61A249_r1_76 (synonym: hairy2) Homo sapiens cDNA clone DKFZp61A249' 5'
							zb53e12.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342' 3'

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6148	16021	26161	1.41	3.4E-01	AJ468082.1	EST_HUMAN	tm63g05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone MAGE:2162840 3' similar to gb:S37431
6943	16821		1.77	3.4E-01	AA337053.1	EST_HUMAN	LAMININ RECEPTOR (HUMAN); EST:41765 Endometrial tumor Homo sapiens cDNA 5' end
7139	17016	27209	1.62	3.4E-01	9633624 NT	Bovine enterovirus strain K2577, complete genome	
7313	17189	27390	3.88	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
7313	17189	27391	3.88	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
7433	16446	28635	4.17	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
7433	16446	28636	4.17	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
7690	17540	27766	2.22	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
8380	18257		4.09	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 101844 to 1029212 (section 87 of 148) of the complete genome
8407	18283	28536	2.2	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN
8440	18314	28572	2.26	3.4E-01	AF045981.1	NT	Rutilus arcasi cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
8604	18471	28742	1.77	3.4E-01	M25556.1	NT	Human von Willebrand factor gene, exons 36 and 37
8604	18471	28743	1.77	3.4E-01	M25556.1	NT	Human von Willebrand factor gene, exons 36 and 37
8790	18605	28895	1.8	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-glycerin/MUC18, complete cds
8814	18627	28916	4.03	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9020	18814		2.01	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
9130	18887		1.3	3.4E-01	Z21621.1	NT	S.cerevisiae RIB5 gene encoding Riboflavin synthase
9229	19508		1.82	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cwf8p (cwf8) gene, complete cds
9347	19024		4.9	3.4E-01	LG26339.1	NT	Human autoantigen mRNA, complete cds
9378	19538		2.49	3.4E-01	BE218652.1	EST_HUMAN	hva2h08>x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone MAGE:3176127 3' similar to contains PTR5.3 PTR5 repetitive element;
9432	19639		2.13	3.4E-01	9838361 NT	Beta vulgaris mitochondrion, complete genome	
9537	19140	25264	1.79	3.4E-01	AJ297131.1	NT	Mus musculus SII, MAP_17, CYP_a, SCL & CYP_b genes
9829	19330						Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W) RD, complement factor B (Bf), and complement component C2 (C2) genes >
14	10000	19791	7.91	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5.11 nodX gene
100	10000	19791	3.92	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5.11 nodX gene
440	10384	20208	1.16	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
617	10554	20366	1.41	3.3E-01	7662485 NT	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1182	11093	20940	3.05	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1285	11193	21046		4.82	3.3E-01	BF688880.1 EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1588	11492	21352		1.11	3.3E-01	67536855 NT	Mus musculus disintegrin 5 (Dign5), mRNA
1704	11605			1.05	3.3E-01	AA332734.1 EST_HUMAN	EST36722 Embryo, 8 week 1 Homo sapiens cDNA 5' end
							Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMP5), mRNA
2355	12235			4.74	3.3E-01	4507834 NT	Bacteriophage phi-YeO3-12 complete genome
2919	12846	22648		2	3.3E-01	A1251805.1 NT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
2982	12910			1.12	3.3E-01	O02743 SWISSPROT	Streptomyces aigilaceus mitramycin biosynthetic genes
3016	12944	22737		1.01	3.3E-01	A007932.2 NT	Homo sapiens MTA1-L1 gene, complete cds
3450	13387	23173		1.14	3.3E-01	AB012922.1 NT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3738	13650	23433		2.17	3.3E-01	O84645 SWISSPROT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 10
3884	13795	23582		1.59	3.3E-01	AL161498.2 NT	Hypoxylon fragiforme chitin synthase gene, partial cds
3920	13829	23609		1.92	3.3E-01	AF20446.1 NT	Rattus norvegicus DNA for regucalcin, partial cds
4271	14170			2.74	3.3E-01	D31662.1 NT	tp78b12.x1 NCI CGAP_U3 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN); R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
4589	14477			1.48	3.3E-01	A1539114.1 EST_HUMAN	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5263	15185	24960		2.68	3.3E-01	X98819.1 NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5263	15185	24961		2.68	3.3E-01	X98819.1 NT	
5622	15537	25623		2.71	3.3E-01	BE619650.1 EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
5622	15537	25624		2.71	3.3E-01	BE619650.1 EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6117	16011	26148		3.64	3.3E-01	AI628131.1 EST_HUMAN	ty84n01.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
6117	16011	26149		3.64	3.3E-01	AI628131.1 EST_HUMAN	ty84n01.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
6575	16483	26616		1.5	3.3E-01	N85146.1 EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
6981	16838	27053		19.46	3.3E-01	BF683854.1 EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
7477	17337	27542		3.26	3.3E-01	N68866.1 EST_HUMAN	za67h01.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297649 3'
7507	17295	27504		2.81	3.3E-01	BF376745.1 EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
7739	17589			2.07	3.3E-01	L41044.1 NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
8104	17994	28242		2.71	3.3E-01	X63953.1 NT	D.mauritiana Adh gene
8104	17994	28243		2.71	3.3E-01	X63953.1 NT	D.mauritiana Adh gene
8389	18265			1.82	3.3E-01	BF526499.1 EST_HUMAN	602070822F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213585 5'
8561	18431	28700		12.76	3.3E-01	BE219351.1 EST_HUMAN	hv51g02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'